Seq. No.	237596
Seq. ID	uC-gsronu33B150g12b1
Method	BLASTX
NCBI GI	g3152585
BLAST score	321
E value	1.0e-29
Match length	134
% identity	53
NCBI Description	(AC002986) Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis thaliana]

Seq. No.	237597
Seq. ID	uC-gsronu33B150h07b1
Method	BLASTX
NCBI GI	g3264830
BLAST score	276
E value	2.0e-24
Match length	128
% identity	53
NCBI Description	(AF072405) cotton fiber expressed protein 2 [Gossypium hirsutum]

Seq. No.	237598
Seq. ID	uC-gsronu33B150h11b1
Method	BLASTX
NCBI GI	g4115371
BLAST score	206
E value	4.0e-16
Match length	81
% identity	78
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	237599
Seq. ID	uC-gsronu33B153b03b2
Method	BLASTX
NCBI GI	g123178
BLAST score	480
E value	1.0e-48
Match length	106
% identity	89
NCBI Description	HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi_99844_pir__A39358 histidinol dehydrogenase (EC 1.1.1.23) precursor, chloroplast - cabbage >gi_167142 (M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No.	237600
Seq. ID	uC-gsronu33B153c01b2
Method	BLASTX
NCBI GI	g461753
BLAST score	586
E value	6.0e-61
Match length	118
% identity	98
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB proteinase regulatory chain homolog precursor, chloroplast

- garden pea >gi_169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

Seq. No.	237601
Seq. ID	uC-gsronu33B153c02b2
Method	BLASTX
NCBI GI	g1903357
BLAST score	384
E value	4.0e-37
Match length	116
% identity	59
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	237602
Seq. ID	uC-gsronu33B153c09b2
Method	BLASTX
NCBI GI	g2924520
BLAST score	470
E value	2.0e-47
Match length	99
% identity	90
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	237603
Seq. ID	uC-gsronu33B153e02b2
Method	BLASTX
NCBI GI	g3603456
BLAST score	493
E value	4.0e-50
Match length	98
% identity	30
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	237604
Seq. ID	uC-gsronu33B153e08b2
Method	BLASTX
NCBI GI	g2213600
BLAST score	160
E value	5.0e-11
Match length	68
% identity	50
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	237605
Seq. ID	uC-gsronu33B153g01b2
Method	BLASTX
NCBI GI	g3915826
BLAST score	191
E value	1.0e-14
Match length	50
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	237606
Seq. ID	uC-gsronu33B153g07b2

Method	BLASTX
NCBI GI	g4490708
BLAST score	223
E value	2.0e-18
Match length	56
% identity	79
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	237607
Seq. ID	uC-gsronu33B153h06b2
Method	BLASTX
NCBI GI	g3935145
BLAST score	253
E value	9.0e-22
Match length	94
% identity	52
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	237608
Seq. ID	uC-gsronu33B153h11b2
Method	BLASTX
NCBI GI	g2244827
BLAST score	231
E value	3.0e-19
Match length	97
% identity	60
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237609
Seq. ID	uC-gsronu33B154a10b2
Method	BLASTX
NCBI GI	g3832528
BLAST score	166
E value	4.0e-12
Match length	59
% identity	59
NCBI Description	(AF100167) unknown [Glycine max]

Seq. No.	237610
Seq. ID	uC-gsronu33B154b08b2
Method	BLASTX
NCBI GI	g1420887
BLAST score	154
E value	3.0e-10
Match length	55
% identity	49
NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	237611
Seq. ID	uC-gsronu33B154c10b2
Method	BLASTX
NCBI GI	g2384696
BLAST score	164
E value	2.0e-11
Match length	66
% identity	48

NCBI Description	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]

Seq. No.	237612
Seq. ID	uC-gsronu33B154d02b2
Method	BLASTX
NCBI GI	g3426039
BLAST score	196
E value	2.0e-15
Match length	53
% identity	66
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	237613
Seq. ID	uC-gsronu33B154d03b2
Method	BLASTX
NCBI GI	g2244975
BLAST score	140
E value	1.0e-08
Match length	57
% identity	53
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237614
Seq. ID	uC-gsronu33B154d08b2
Method	BLASTX
NCBI GI	g2245131
BLAST score	325
E value	3.0e-30
Match length	112
% identity	64
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237615
Seq. ID	uC-gsronu33B154e03b2
Method	BLASTX
NCBI GI	g3892056
BLAST score	208
E value	2.0e-16
Match length	48
% identity	88
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	237616
Seq. ID	uC-gsronu33B154e06b2
Method	BLASTX
NCBI GI	g1172004
BLAST score	726
E value	3.0e-77
Match length	154
% identity	93
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi_1345583_emb_CAA53581_ (X75967) phenylalanine ammonium lyase [Vitis vinifera]

Seq. No.	237617
Seq. ID	uC-gsronu33B154e08b2
Method	BLASTX
NCBI GI	g3395432

BLAST score	299
E value	3.0e-27
Match length	105
% identity	59
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	237618
Seq. ID	uC-gsronu33B154f04b2
Method	BLASTX
NCBI GI	g2245094
BLAST score	304
E value	1.0e-27
Match length	148
% identity	45
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237619
Seq. ID	uC-gsronu33B154f09b2
Method	BLASTX
NCBI GI	g1657948
BLAST score	293
E value	1.0e-26
Match length	59
% identity	92
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	237620
Seq. ID	uC-gsronu33B154g06b2
Method	BLASTX
NCBI GI	g1332579
BLAST score	594
E value	9.0e-62
Match length	120
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	237621
Seq. ID	uC-gsronu33B155a06b2
Method	BLASTX
NCBI GI	g115492
BLAST score	438
E value	1.0e-43
Match length	85
% identity	50
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]

Seq. No.	237622
Seq. ID	uC-gsronu33B155a09b2
Method	BLASTX
NCBI GI	g2252856
BLAST score	292
E value	2.0e-26
Match length	130
% identity	52
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	237623
Seq. ID	uC-gsronu33B155a11b2
Method	BLASTX
NCBI GI	g2252839
BLAST score	465
E value	8.0e-47
Match length	97
% identity	88
NCBI Description	(AF013293) Similar to receptor-like protein kinase precusor [Arabidopsis thaliana]

Seq. No.	237624
Seq. ID	uC-gsronu33B155b05b2
Method	BLASTX
NCBI GI	g2924258
BLAST score	621
E value	6.0e-65
Match length	131
% identity	90
NCBI Description	(Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No.	237625
Seq. ID	uC-gsronu33B155b12b2
Method	BLASTX
NCBI GI	g4164159
BLAST score	666
E value	5.0e-70
Match length	169
% identity	82
NCBI Description	(AB015496) ethylene receptor [Passiflora edulis]

Seq. No.	237626
Seq. ID	uC-gsronu33B155c11b2
Method	BLASTX
NCBI GI	g1755166
BLAST score	309
E value	2.0e-28
Match length	83
% identity	71
NCBI Description	(U75194) germin-like protein [Arabidopsis thaliana]

Seq. No.	237627
Seq. ID	uC-gsronu33B155f01b2
Method	BLASTX
NCBI GI	g4220512
BLAST score	467
E value	4.0e-47
Match length	99
% identity	83
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	237628
Seq. ID	uC-gsronu33B155f07b2
Method	BLASTX
NCBI GI	g3641868
BLAST score	292
E value	3.0e-26

Match length	86
% identity	69
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]

Seq. No.	237629
Seq. ID	uC-gsronu33B155g07b2
Method	BLASTX
NCBI GI	g484656
BLAST score	186
E value	5.0e-14
Match length	51
% identity	69
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi_452165_dbj_BAA05408_ (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	237630
Seq. ID	uC-gsronu33B155g09b2
Method	BLASTX
NCBI GI	g3551247
BLAST score	160
E value	9.0e-11
Match length	32
% identity	94
NCBI Description	(AB012703) 181 [Daucus carota]

Seq. No.	237631
Seq. ID	uC-gsronu33B155h10b2
Method	BLASTX
NCBI GI	g2765837
BLAST score	176
E value	1.0e-12
Match length	42
% identity	79
NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No.	237632
Seq. ID	uC-gsronu33B156b08b1
Method	BLASTX
NCBI GI	g2130080
BLAST score	264
E value	2.0e-27
Match length	130
% identity	43
NCBI Description	Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

Seq. No.	237633
Seq. ID	uC-gsronu33B156c05b1
Method	BLASTX
NCBI GI	g3493172
BLAST score	149
E value	4.0e-10
Match length	27

% identity	100
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]

Seq. No.	237634
Seq. ID	uC-gsronu33B156d11b1
Method	BLASTX
NCBI GI	g1279588
BLAST score	468
E value	7.0e-47
Match length	146
% identity	62
NCBI Description	(Z71749) glutathione S-transferase [Nicotiana plumbaginifolia]

Seq. No.	237635
Seq. ID	uC-gsronu33B156d12b1
Method	BLASTX
NCBI GI	g2213586
BLAST score	200
E value	1.0e-15
Match length	83
% identity	49
NCBI Description	(AC000348) T7N9.6 [Arabidopsis thaliana]

Seq. No.	237636
Seq. ID	uC-gsronu33B156e01b1
Method	BLASTX
NCBI GI	g3135274
BLAST score	263
E value	6.0e-23
Match length	123
% identity	46
NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	237637
Seq. ID	uC-gsronu33B156f11b1
Method	BLASTX
NCBI GI	g465820
BLAST score	473
E value	1.0e-47
Match length	124
% identity	67
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi_280536_pir__S28301 hypothetical protein C40H1.6 - Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154) C40H1.6 [Caenorhabditis elegans]

Seq. No.	237638
Seq. ID	uC-gsronu33B157a03b1
Method	BLASTX
NCBI GI	g1370174
BLAST score	282
E value	4.0e-25
Match length	60
% identity	88
NCBI Description	(Z73936) RAB1Y [Lotus japonicus]

Seq. No.	237639
Seq. ID	uC-gsronu33B157d09b1
Method	BLASTX
NCBI GI	g3786008
BLAST score	282
E value	3.0e-25
Match length	111
% identity	50
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	237640
Seq. ID	uC-gsronu33B157f11b1
Method	BLASTX
NCBI GI	g4006870
BLAST score	439
E value	2.0e-43
Match length	175
% identity	49
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	237641
Seq. ID	uC-gsronu33B158a12b2
Method	BLASTX
NCBI GI	g1684855
BLAST score	323
E value	5.0e-30
Match length	69
% identity	20
NCBI Description	(U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No.	237642
Seq. ID	uC-gsronu33B158b03b2
Method	BLASTX
NCBI GI	g398966
BLAST score	607
E value	3.0e-63
Match length	135
% identity	85
NCBI Description	4-COUMARATE--COA LIGASE 2 (4CL) (CLONE 4CL16) >gi_541937_pir__PQ0772 4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL1B) - soybean (fragment) >gi_18520_emb_CAA49576_ (X69955) 4-coumarate--CoA ligase [Glycine max]

Seq. No.	237643
Seq. ID	uC-gsronu33B158b04b2
Method	BLASTX
NCBI GI	g4138583
BLAST score	165
E value	2.0e-11
Match length	87
% identity	56
NCBI Description	(Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No.	237644
Seq. ID	uC-gsronu33B158b06b2

Method	BLASTX
NCBI GI	g3024148
BLAST score	411
E value	1.0e-40
Match length	86
% identity	90
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1655580_emb_CAA95858_ (Z71273) S-adenosyl-L-methionine synthetase 3 [Catharanthus roseus]

Seq. No.	237645
Seq. ID	uC-gsronu33B158b08b2
Method	BLASTX
NCBI GI	g4204277
BLAST score	138
E value	8.0e-09
Match length	56
% identity	54
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	237646
Seq. ID	uC-gsronu33B158c03b2
Method	BLASTX
NCBI GI	g294668
BLAST score	403
E value	1.0e-39
Match length	100
% identity	79
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	237647
Seq. ID	uC-gsronu33B158d01b2
Method	BLASTX
NCBI GI	g4191788
BLAST score	418
E value	4.0e-41
Match length	99
% identity	76
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No.	237648
Seq. ID	uC-gsronu33B158d09b2
Method	BLASTX
NCBI GI	g2894379
BLAST score	205
E value	5.0e-16
Match length	90
% identity	47
NCBI Description	(Y14573) ring finger protein [Hordeum vulgare]

Seq. No.	237649
Seq. ID	uC-gsronu33B158d10b2
Method	BLASTX
NCBI GI	g2388689
BLAST score	456

E value	2.0e-45
Match length	123
% identity	73
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	237650
Seq. ID	uC-gsronu33B158e11b2
Method	BLASTX
NCBI GI	g3123349
BLAST score	179
E value	2.0e-13
Match length	57
% identity	63
NCBI Description	(AJ005788) hypothetical protein [Cicer arietinum]

Seq. No.	237651
Seq. ID	uC-gsronu33B158f01b2
Method	BLASTX
NCBI GI	g2582800
BLAST score	516
E value	1.0e-52
Match length	119
% identity	82
NCBI Description	(Y11607) protein phosphatase 2C [Medicago sativa]

Seq. No.	237652
Seq. ID	uC-gsronu33B158g02b2
Method	BLASTX
NCBI GI	g3193332
BLAST score	277
E value	3.0e-25
Match length	60
% identity	90
NCBI Description	(AF069299) similar to Arabidopsis AT-hook protein 1 (GB:AJ222585) [Arabidopsis thaliana]

Seq. No.	237653
Seq. ID	uC-gsronu33B158g08b2
Method	BLASTX
NCBI GI	g2281090
BLAST score	190
E value	6.0e-15
Match length	51
% identity	73
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237654
Seq. ID	uC-gsronu33B158h08b2
Method	BLASTX
NCBI GI	g1929056
BLAST score	183
E value	7.0e-14
Match length	63
% identity	56
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	237655
Seq. ID	uC-gsronu33B158h12b2
Method	BLASTX
NCBI GI	g2160756
BLAST score	455
E value	2.0e-45
Match length	139
% identity	11
NCBI Description	(U96879) CLV1 receptor kinase [Arabidopsis thaliana]

Seq. No.	237656
Seq. ID	uC-gsronu33B159a03b1
Method	BLASTX
NCBI GI	g2673915
BLAST score	298
E value	2.0e-36
Match length	111
% identity	65
NCBI Description	(AC002561) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	237657
Seq. ID	uC-gsronu33B159b07b1
Method	BLASTX
NCBI GI	g4510428
BLAST score	349
E value	1.0e-36
Match length	122
% identity	60
NCBI Description	(AC006929) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	237658
Seq. ID	uC-gsronu33B159b10b1
Method	BLASTX
NCBI GI	g2341039
BLAST score	486
E value	5.0e-49
Match length	141
% identity	67
NCBI Description	(AC000104) Similar to Nicotiana lesion-inducing ORF (gb_U66269). [Arabidopsis thaliana]

Seq. No.	237659
Seq. ID	uC-gsronu33B159d11b1
Method	BLASTX
NCBI GI	g3043432
BLAST score	284
E value	2.0e-25
Match length	54
% identity	100
NCBI Description	(AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

Seq. No.	237660
Seq. ID	uC-gsronu33B159e01b1
Method	BLASTX
NCBI GI	g2129770
BLAST score	285

E value	2.0e-25
Match length	87
% identity	61
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]
Seq. No.	237661
Seq. ID	uC-gsronu33B159f04b1
Method	BLASTX
NCBI GI	g1363492
BLAST score	817
E value	9.0e-88
Match length	173
% identity	88
NCBI Description	outer envelope membrane protein OEP75 precursor - garden pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]
Seq. No.	237662
Seq. ID	uC-gsronu33B159g08b1
Method	BLASTX
NCBI GI	g4234953
BLAST score	191
E value	2.0e-14
Match length	97
% identity	24
NCBI Description	(AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]
Seq. No.	237663
Seq. ID	uC-gsronu33B159g10b1
Method	BLASTX
NCBI GI	g4206789
BLAST score	206
E value	4.0e-16
Match length	67
% identity	60
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]
Seq. No.	237664
Seq. ID	uC-gsronu33B159h09b1
Method	BLASTX
NCBI GI	g4539314
BLAST score	158
E value	1.0e-17
Match length	82
% identity	62
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]
Seq. No.	237665
Seq. ID	uC-gsronu33B160a03b1
Method	BLASTX
NCBI GI	g1762945

BLAST score 300
E value 4.0e-27
Match length 92
% identity 58
NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No. 237666
Seq. ID uC-gsronu33B160a04b1
Method BLASTX
NCBI GI g4530126
BLAST score 504
E value 4.0e-51
Match length 162
% identity 57
NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No. 237667
Seq. ID uC-gsronu33B160b04b1
Method BLASTX
NCBI GI g4510402
BLAST score 601
E value 1.0e-62
Match length 139
% identity 51
NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]

Seq. No. 237668
Seq. ID uC-gsronu33B160b05b1
Method BLASTX
NCBI GI g4335763
BLAST score 286
E value 1.0e-25
Match length 106
% identity 52
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 237669
Seq. ID uC-gsronu33B160c04b1
Method BLASTX
NCBI GI g3687251
BLAST score 361
E value 3.0e-34
Match length 95
% identity 75
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 237670
Seq. ID uC-gsronu33B160d08b1
Method BLASTX
NCBI GI g1708073
BLAST score 416
E value 8.0e-41
Match length 151
% identity 57
NCBI Description GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE

AMIDOTRANSFERASE) (GMP SYNTHETASE) >gi_1077145_pir__S55099 GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) - yeast (Saccharomyces cerevisiae) >gi_854469_emb_CAA89932_ (Z49809) Gua1p [Saccharomyces cerevisiae]

Seq. No.	237671
Seq. ID	uC-gsronu33B160d11b1
Method	BLASTX
NCBI GI	g114171
BLAST score	240
E value	3.0e-20
Match length	48
% identity	90
NCBI Description	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR (3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) >gi_99781_pir__S12744 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - rape >gi_17815_emb_CAA35839_ (X51475) 5-enolpyruvylshikimate-3-phosphate synthase [Brassica napus]

Seq. No.	237672
Seq. ID	uC-gsronu33B160e01b1
Method	BLASTX
NCBI GI	g2462746
BLAST score	217
E value	1.0e-17
Match length	47
% identity	85
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	237673
Seq. ID	uC-gsronu33B160e11b1
Method	BLASTX
NCBI GI	g3114901
BLAST score	410
E value	5.0e-40
Match length	101
% identity	78
NCBI Description	(AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] >gi_3114905_emb_CAA06709_ (AJ005806) pceberh [Populus balsamifera subsp. trichocarpa]

Seq. No.	237674
Seq. ID	uC-gsronu33B160f03b1
Method	BLASTX
NCBI GI	g3157924
BLAST score	164
E value	2.0e-11
Match length	57
% identity	56
NCBI Description	(AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like

protein [Arabidopsis thaliana]

Seq. No.	237675
Seq. ID	uC-gsronu33B160f07b1
Method	BLASTX
NCBI GI	g1907076
BLAST score	389
E value	9.0e-38
Match length	113
% identity	63
NCBI Description	(Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_ (Y07868) pirin [Homo sapiens] >gi_4505823_ref_NP_003653.1_pPIR_ pirin

Seq. No.	237676
Seq. ID	uC-gsronu33B162a03b2
Method	BLASTX
NCBI GI	g4539348
BLAST score	297
E value	2.0e-27
Match length	76
% identity	72
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	237677
Seq. ID	uC-gsronu33B162a07b2
Method	BLASTX
NCBI GI	g557472
BLAST score	172
E value	2.0e-12
Match length	84
% identity	42
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	237678
Seq. ID	uC-gsronu33B162b04b2
Method	BLASTX
NCBI GI	g4455323
BLAST score	259
E value	1.0e-22
Match length	117
% identity	48
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	237679
Seq. ID	uC-gsronu33B162d02b2
Method	BLASTX
NCBI GI	g4006878
BLAST score	317
E value	3.0e-29
Match length	120
% identity	54
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	237680
Seq. ID	uC-gsronu33B162e05b2

Method	BLASTX
NCBI GI	g2226436
BLAST score	225
E value	2.0e-18
Match length	122
% identity	43
NCBI Description	(L39907) LA-MSC [Oxytricha fallax]

Seq. No.	237681
Seq. ID	uC-gsronu33B162e07b2
Method	BLASTX
NCBI GI	g439493
BLAST score	257
E value	3.0e-22
Match length	138
% identity	36
NCBI Description	(D26086) zinc-finger protein [Petunia x hybrida]

Seq. No.	237682
Seq. ID	uC-gsronu33B162e11b2
Method	BLASTX
NCBI GI	g3063449
BLAST score	558
E value	2.0e-57
Match length	159
% identity	70
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	237683
Seq. ID	uC-gsronu33B162f08b2
Method	BLASTX
NCBI GI	g4371296
BLAST score	152
E value	6.0e-10
Match length	125
% identity	34
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	237684
Seq. ID	uC-gsronu33B162f09b2
Method	BLASTX
NCBI GI	g2832619
BLAST score	279
E value	9.0e-25
Match length	80
% identity	69
NCBI Description	(AL021711) major intrinsic protein (MIP)- like [Arabidopsis thaliana]

Seq. No.	237685
Seq. ID	uC-gsronu33B162f12b2
Method	BLASTX
NCBI GI	g4140371
BLAST score	403
E value	3.0e-39
Match length	95

% identity	85
NCBI Description	(U43711) 3-hydroxy-3-methylglutaryl-coenzyme A reductase [Morus alba]

Seq. No.	237686
Seq. ID	uC-gsronu33B162h08b2
Method	BLASTX
NCBI GI	g4049399
BLAST score	167
E value	3.0e-22
Match length	117
% identity	55
NCBI Description	(Y09581) FRO2 [Arabidopsis thaliana]

Seq. No.	237687
Seq. ID	uC-gsronu33B163a11b2
Method	BLASTX
NCBI GI	g120669
BLAST score	390
E value	3.0e-38
Match length	80
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	237688
Seq. ID	uC-gsronu33B163b11b2
Method	BLASTX
NCBI GI	g2315153
BLAST score	288
E value	3.0e-26
Match length	88
% identity	58
NCBI Description	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]

Seq. No.	237689
Seq. ID	uC-gsronu33B163c05b2
Method	BLASTX
NCBI GI	g2829911
BLAST score	505
E value	2.0e-51
Match length	121
% identity	43
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	237690
Seq. ID	uC-gsronu33B163c06b2
Method	BLASTX
NCBI GI	g3786005
BLAST score	545
E value	5.0e-56
Match length	126
% identity	44
NCBI Description	(AC005499) putative phosphoethanolamine

cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	237691
Seq. ID	uC-gsronu33B163c09b2
Method	BLASTX
NCBI GI	g2642158
BLAST score	441
E value	6.0e-44
Match length	118
% identity	70
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237692
Seq. ID	uC-gsronu33B163d01b2
Method	BLASTX
NCBI GI	g1840425
BLAST score	322
E value	6.0e-30
Match length	79
% identity	72
NCBI Description	(U36586) alcohol dehydrogenase [Vitis vinifera]

Seq. No.	237693
Seq. ID	uC-gsronu33B163d03b2
Method	BLASTX
NCBI GI	g3005576
BLAST score	347
E value	6.0e-33
Match length	86
% identity	76
NCBI Description	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No.	237694
Seq. ID	uC-gsronu33B163d08b2
Method	BLASTX
NCBI GI	g4557078
BLAST score	283
E value	1.0e-27
Match length	166
% identity	42
NCBI Description	(AC007045) putative Tal1-1 pol polyprotein, 5' partial [Arabidopsis thaliana]

Seq. No.	237695
Seq. ID	uC-gsronu33B163e11b2
Method	BLASTX
NCBI GI	g3152618
BLAST score	406
E value	8.0e-40
Match length	115
% identity	65
NCBI Description	(AC004482) putative pectinesterase [Arabidopsis thaliana] >gi_3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 237696

Seq. ID	uC-gsronu33B163f02b2
Method	BLASTX
NCBI GI	g1644291
BLAST score	158
E value	1.0e-10
Match length	116
% identity	32
NCBI Description	(Z73295) receptor-like protein kinase [Catharanthus roseus]

Seq. No.	237697
Seq. ID	uC-gsronu33B163f04b2
Method	BLASTX
NCBI GI	g2245108
BLAST score	540
E value	2.0e-55
Match length	136
% identity	73
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	237698
Seq. ID	uC-gsronu33B163g11b2
Method	BLASTX
NCBI GI	g99737
BLAST score	225
E value	2.0e-18
Match length	76
% identity	59
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	237699
Seq. ID	uC-gsronu33B163h03b2
Method	BLASTX
NCBI GI	g4512673
BLAST score	782
E value	1.0e-83
Match length	157
% identity	92
NCBI Description	(AC006931) putative phosphoprotein phosphatase [Arabidopsis thaliana]

Seq. No.	237700
Seq. ID	uC-gsronu33B164a01b2
Method	BLASTX
NCBI GI	g3283912
BLAST score	226
E value	1.0e-18
Match length	112
% identity	38
NCBI Description	(AF070639) unknown [Homo sapiens]

Seq. No.	237701
Seq. ID	uC-gsronu33B164c10b2
Method	BLASTX
NCBI GI	g3335359
BLAST score	416

E value	6.0e-41
Match length	124
% identity	64
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	237702
Seq. ID	uC-gsronu33B164c11b2
Method	BLASTX
NCBI GI	g3152618
BLAST score	409
E value	5.0e-40
Match length	123
% identity	56
NCBI Description	(AC004482) putative pectinesterase [Arabidopsis thaliana] >gi_3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	237703
Seq. ID	uC-gsronu33B164e06b2
Method	BLASTX
NCBI GI	g4455223
BLAST score	409
E value	5.0e-40
Match length	115
% identity	27
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	237704
Seq. ID	uC-gsronu33B164e11b2
Method	BLASTX
NCBI GI	g1234787
BLAST score	142
E value	1.0e-08
Match length	145
% identity	32
NCBI Description	(U37373) up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region [Xenopus laevis]

Seq. No.	237705
Seq. ID	uC-gsronu33B164f07b2
Method	BLASTX
NCBI GI	g2598599
BLAST score	288
E value	6.0e-26
Match length	82
% identity	66
NCBI Description	(Y15372) MtN4 [Medicago truncatula]

Seq. No.	237706
Seq. ID	uC-gsronu33B164g01b2
Method	BLASTX
NCBI GI	g2464905
BLAST score	279
E value	6.0e-25

Match length 80
% identity 68
NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]

Seq. No. 237707
Seq. ID uC-gsronu33B164g10b2
Method BLASTX
NCBI GI g2980788
BLAST score 225
E value 2.0e-18
Match length 129
% identity 43
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 237708
Seq. ID uC-gsronu33B166a01b2
Method BLASTX
NCBI GI g4567278
BLAST score 224
E value 2.0e-18
Match length 117
% identity 55
NCBI Description (AC006841) putative anthracycline associated resistance ARX protein [Arabidopsis thaliana]

Seq. No. 237709
Seq. ID uC-gsronu33B166a06b2
Method BLASTX
NCBI GI g3757514
BLAST score 567
E value 1.0e-58
Match length 123
% identity 90
NCBI Description (AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No. 237710
Seq. ID uC-gsronu33B166b02b2
Method BLASTX
NCBI GI g2194118
BLAST score 207
E value 2.0e-16
Match length 71
% identity 49
NCBI Description (AC002062) F20P5.4 gene product [Arabidopsis thaliana]

Seq. No. 237711
Seq. ID uC-gsronu33B166d04b2
Method BLASTX
NCBI GI g2982283
BLAST score 357
E value 7.0e-34
Match length 135
% identity 47
NCBI Description (AF051226) PREG-like protein [Picea mariana]

Seq. No. 237712

Seq. ID	uC-gsronu33B166d08b2
Method	BLASTX
NCBI GI	g4262151
BLAST score	544
E value	6.0e-56
Match length	130
% identity	78
NCBI Description	(AC005275) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	237713
Seq. ID	uC-gsronu33B166d11b2
Method	BLASTX
NCBI GI	g4220482
BLAST score	442
E value	8.0e-44
Match length	121
% identity	45
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237714
Seq. ID	uC-gsronu33B166f11b2
Method	BLASTX
NCBI GI	g466044
BLAST score	166
E value	2.0e-11
Match length	50
% identity	58
NCBI Description	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis elegans >gi_304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]

Seq. No.	237715
Seq. ID	uC-gsronu33B167a04b1
Method	BLASTX
NCBI GI	g2129854
BLAST score	454
E value	2.0e-45
Match length	130
% identity	65
NCBI Description	early nodulin 8 precursor - alfalfa >gi_304037 (L18899) early nodulin [Medicago sativa]

Seq. No.	237716
Seq. ID	uC-gsronu33B167a07b1
Method	BLASTX
NCBI GI	g2497743
BLAST score	178
E value	4.0e-13
Match length	35
% identity	94
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	237717
Seq. ID	uC-gsronu33B167c01b1
Method	BLASTX
NCBI GI	g497896
BLAST score	330
E value	1.0e-30
Match length	151
% identity	54
NCBI Description	(D12921) transcription factor HBP-1b(c1) [Triticum aestivum]

Seq. No.	237718
Seq. ID	uC-gsronu33B167c08b1
Method	BLASTX
NCBI GI	g3600054
BLAST score	144
E value	5.0e-09
Match length	83
% identity	37
NCBI Description	(AF080120) No definition line found [Arabidopsis thaliana]

Seq. No.	237719
Seq. ID	uC-gsronu33B167c12b1
Method	BLASTX
NCBI GI	g4262222
BLAST score	517
E value	1.0e-52
Match length	125
% identity	76
NCBI Description	(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]

Seq. No.	237720
Seq. ID	uC-gsronu33B167d04b1
Method	BLASTX
NCBI GI	g2317906
BLAST score	292
E value	2.0e-26
Match length	62
% identity	97
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	237721
Seq. ID	uC-gsronu33B167e03b1
Method	BLASTX
NCBI GI	g3885340
BLAST score	224
E value	6.0e-19
Match length	68
% identity	65
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	237722
Seq. ID	uC-gsronu33B167f05b1
Method	BLASTX
NCBI GI	g3548810
BLAST score	373

E value	9.0e-36
Match length	144
% identity	57
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	237723
Seq. ID	uC-gsronu33B167h04b1
Method	BLASTX
NCBI GI	g629561
BLAST score	328
E value	2.0e-30
Match length	138
% identity	54
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	237724
Seq. ID	uC-gsronu33B168a05b1
Method	BLASTX
NCBI GI	g3157950
BLAST score	413
E value	2.0e-40
Match length	147
% identity	58
NCBI Description	(AC002131) Contains similarity to hypothetical protein C18b11.05 gb_Z50728 from S. pombe. EST gb_H76601 comes from this gene. [Arabidopsis thaliana]

Seq. No.	237725
Seq. ID	uC-gsronu33B168a07b1
Method	BLASTX
NCBI GI	g2570338
BLAST score	401
E value	4.0e-39
Match length	125
% identity	60
NCBI Description	(U90927) glyoxalase II isozyme [Arabidopsis thaliana]

Seq. No.	237726
Seq. ID	uC-gsronu33B168a09b1
Method	BLASTX
NCBI GI	g81857
BLAST score	170
E value	3.0e-12
Match length	33
% identity	91
NCBI Description	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No.	237727
Seq. ID	uC-gsronu33B168a12b1
Method	BLASTX
NCBI GI	g3142293
BLAST score	142

E value	1.0e-08
Match length	43
% identity	60
NCBI Description	(AC002411) Contains similarity to myosin IB heavy chain gb_X70400 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	237728
Seq. ID	uC-gsronu33B168c01b1
Method	BLASTX
NCBI GI	g3402673
BLAST score	389
E value	9.0e-38
Match length	123
% identity	62
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	237729
Seq. ID	uC-gsronu33B168c03b1
Method	BLASTX
NCBI GI	g417060
BLAST score	618
E value	2.0e-64
Match length	119
% identity	94
NCBI Description	GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi_1094850_prf__2106409A Gln synthetase [Vigna aconitifolia]

Seq. No.	237730
Seq. ID	uC-gsronu33B168d04b1
Method	BLASTX
NCBI GI	g4335745
BLAST score	191
E value	2.0e-14
Match length	84
% identity	49
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	237731
Seq. ID	uC-gsronu33B168d05b1
Method	BLASTX
NCBI GI	g3281861
BLAST score	541
E value	1.0e-55
Match length	132
% identity	77
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	237732
Seq. ID	uC-gsronu33B168e09b1
Method	BLASTX
NCBI GI	g548702
BLAST score	387
E value	2.0e-37

Match length	111
% identity	59
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9) (RPB14.5) >gi_543001_pir__S41621 DNA-directed RNA polymerase (EC 2.7.7.6) II 14.5K chain - human >gi_397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit 14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo sapiens]

Seq. No.	237733
Seq. ID	uC-gsronu33B168f02b1
Method	BLASTX
NCBI GI	g2281090
BLAST score	221
E value	5.0e-18
Match length	141
% identity	37
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237734
Seq. ID	uC-gsronu33B168f03b1
Method	BLASTX
NCBI GI	g4204793
BLAST score	606
E value	4.0e-63
Match length	136
% identity	43
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum]

Seq. No.	237735
Seq. ID	uC-gsronu33B168f12b1
Method	BLASTX
NCBI GI	g4200165
BLAST score	612
E value	8.0e-64
Match length	139
% identity	76
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	237736
Seq. ID	uC-gsronu33B168g07b1
Method	BLASTX
NCBI GI	g3914685
BLAST score	294
E value	8.0e-27
Match length	91
% identity	64
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No.	237737
Seq. ID	uC-gsronu33B168g08b1
Method	BLASTX
NCBI GI	g2832617
BLAST score	164
E value	3.0e-11

Match length	92
% identity	43
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	237738
Seq. ID	uC-gsronu33B168g09b1
Method	BLASTX
NCBI GI	g3309243
BLAST score	597
E value	4.0e-62
Match length	125
% identity	91
NCBI Description	(AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No.	237739
Seq. ID	uC-gsronu33B168g12b1
Method	BLASTX
NCBI GI	g3122914
BLAST score	175
E value	1.0e-12
Match length	63
% identity	52
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	237740
Seq. ID	uC-gsronu33B168h10b1
Method	BLASTX
NCBI GI	g541848
BLAST score	444
E value	4.0e-44
Match length	146
% identity	52
NCBI Description	amino acid transport protein I - Arabidopsis thaliana >gi_22641_emb_CAA47603_ (X67124) amino acid permease I [Arabidopsis thaliana] >gi_404019 (L16240) amino acid transporter [Arabidopsis thaliana]

Seq. No.	237741
Seq. ID	uC-gsronu33B169a07b1
Method	BLASTX
NCBI GI	g2341024
BLAST score	384
E value	6.0e-37
Match length	127
% identity	39
NCBI Description	(AC000104) F19P19.1 [Arabidopsis thaliana]

Seq. No.	237742
Seq. ID	uC-gsronu33B169a10b1
Method	BLASTX
NCBI GI	g282848
BLAST score	586
E value	9.0e-61
Match length	143

% identity	82
NCBI Description	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) (clone 064) - western balsam poplar x cottonwood
Seq. No.	237743
Seq. ID	uC-gsronu33B169b03b1
Method	BLASTX
NCBI GI	g4115381
BLAST score	217
E value	2.0e-17
Match length	86
% identity	52
NCBI Description	(AC005967) putative limonene cyclase [Arabidopsis thaliana]
Seq. No.	237744
Seq. ID	uC-gsronu33B169b08b1
Method	BLASTX
NCBI GI	g218157
BLAST score	378
E value	2.0e-36
Match length	85
% identity	88
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]
Seq. No.	237745
Seq. ID	uC-gsronu33B169b09b1
Method	BLASTX
NCBI GI	g4220481
BLAST score	506
E value	2.0e-51
Match length	134
% identity	71
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.	237746
Seq. ID	uC-gsronu33B169c04b1
Method	BLASTX
NCBI GI	g1345644
BLAST score	314
E value	5.0e-29
Match length	83
% identity	69
NCBI Description	CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446_emb_CAA62082_ (X90458) cytochrome p450 [Arabidopsis thaliana]
Seq. No.	237747
Seq. ID	uC-gsronu33B169c11b1
Method	BLASTX
NCBI GI	g4006888
BLAST score	668
E value	3.0e-70
Match length	172
% identity	71
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	237748

Seq. ID	uC-gsronu33B169d04b1
Method	BLASTX
NCBI GI	g1173187
BLAST score	412
E value	2.0e-40
Match length	81
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	237749
Seq. ID	uC-gsronu33B169d08b1
Method	BLASTX
NCBI GI	g2232354
BLAST score	247
E value	6.0e-21
Match length	155
% identity	41
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	237750
Seq. ID	uC-gsronu33B169d10b1
Method	BLASTX
NCBI GI	g3790569
BLAST score	340
E value	7.0e-32
Match length	130
% identity	54
NCBI Description	(AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No.	237751
Seq. ID	uC-gsronu33B169e08b1
Method	BLASTX
NCBI GI	g1184123
BLAST score	234
E value	2.0e-19
Match length	79
% identity	56
NCBI Description	(U20809) auxin-induced protein [Vigna radiata]

Seq. No.	237752
Seq. ID	uC-gsronu33B169f07b1
Method	BLASTX
NCBI GI	g4006818
BLAST score	165
E value	2.0e-11
Match length	70
% identity	47
NCBI Description	(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]

Seq. No.	237753
Seq. ID	uC-gsronu33B169h11b1
Method	BLASTX

NCBI GI g1669599
BLAST score 327
E value 2.0e-30
Match length 130
% identity 53
NCBI Description (D88746) AR791 [Arabidopsis thaliana]

Seq. No. 237754
Seq. ID uC-gsronu33B170a12b1
Method BLASTX
NCBI GI g1616628
BLAST score 220
E value 6.0e-18
Match length 106
% identity 51
NCBI Description (X80472) sts15 [Solanum tuberosum]

Seq. No. 237755
Seq. ID uC-gsronu33B170b08b1
Method BLASTX
NCBI GI g3927829
BLAST score 298
E value 7.0e-27
Match length 164
% identity 43
NCBI Description (AC005727) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 237756
Seq. ID uC-gsronu33B170c01b1
Method BLASTX
NCBI GI g2911076
BLAST score 388
E value 1.0e-37
Match length 99
% identity 74
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 237757
Seq. ID uC-gsronu33B170c03b1
Method BLASTX
NCBI GI g4567313
BLAST score 151
E value 1.0e-09
Match length 34
% identity 74
NCBI Description (AC005956) putative SUPERMAN transcription factor [Arabidopsis thaliana]

Seq. No. 237758
Seq. ID uC-gsronu33B170f01b1
Method BLASTX
NCBI GI g3269283
BLAST score 148
E value 2.0e-09
Match length 135
% identity 30

NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]
Seq. No.	237759
Seq. ID	uC-gsronu33B170f09b1
Method	BLASTX
NCBI GI	g1703478
BLAST score	708
E value	5.0e-75
Match length	157
% identity	47
NCBI Description	(U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana]
Seq. No.	237760
Seq. ID	uC-gsronu33B170h02b1
Method	BLASTX
NCBI GI	g4580392
BLAST score	177
E value	1.0e-15
Match length	130
% identity	41
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237761
Seq. ID	uC-gsronu33B171a01b1
Method	BLASTX
NCBI GI	g4539389
BLAST score	183
E value	4.0e-14
Match length	49
% identity	76
NCBI Description	(AL035526) putative protein kinase [Arabidopsis thaliana]
Seq. No.	237762
Seq. ID	uC-gsronu33B171c05b1
Method	BLASTX
NCBI GI	g266972
BLAST score	143
E value	4.0e-09
Match length	35
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens] >gi_4506717_ref_NP_001023.1_pRPS29_ ribosomal protein S29
Seq. No.	237763
Seq. ID	uC-gsronu33B171d12b1
Method	BLASTX
NCBI GI	g4544464

BLAST score	423
E value	7.0e-42
Match length	94
% identity	70
NCBI Description	(AC006580) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	237764
Seq. ID	uC-gsronu33B171e09b1
Method	BLASTX
NCBI GI	g1076511
BLAST score	576
E value	1.0e-59
Match length	123
% identity	95
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	237765
Seq. ID	uC-gsronu33B172a08b1
Method	BLASTX
NCBI GI	g2252836
BLAST score	167
E value	9.0e-12
Match length	109
% identity	38
NCBI Description	(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]

Seq. No.	237766
Seq. ID	uC-gsronu33B172b05b1
Method	BLASTX
NCBI GI	g547683
BLAST score	144
E value	3.0e-09
Match length	37
% identity	89
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	237767
Seq. ID	uC-gsronu33B172b06b1
Method	BLASTX
NCBI GI	g2129651
BLAST score	166
E value	7.0e-12
Match length	48
% identity	69
NCBI Description	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana]

Seq. No.	237768
Seq. ID	uC-gsronu33B172b07b1

Method	BLASTX
NCBI GI	g232278
BLAST score	307
E value	4.0e-28
Match length	115
% identity	63
NCBI Description	CHLOROPLAST SMALL HEAT SHOCK PROTEIN PRECURSOR >gi_100397_pir__S16004 heat shock protein 21 - garden petunia >gi_14158_emb_CAA38037_ (X54103) heat shock protein [Petunia x hybrida]

Seq. No.	237769
Seq. ID	uC-gsronu33B172c03b1
Method	BLASTX
NCBI GI	g3763921
BLAST score	322
E value	8.0e-30
Match length	84
% identity	74
NCBI Description	(AC004450) putative pirin protein [Arabidopsis thaliana]

Seq. No.	237770
Seq. ID	uC-gsronu33B172d09b1
Method	BLASTX
NCBI GI	g4559384
BLAST score	156
E value	2.0e-10
Match length	43
% identity	70
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	237771
Seq. ID	uC-gsronu33B172e04b1
Method	BLASTX
NCBI GI	g3785989
BLAST score	188
E value	3.0e-14
Match length	41
% identity	85
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	237772
Seq. ID	uC-gsronu33B172f06b1
Method	BLASTX
NCBI GI	g4098129
BLAST score	370
E value	2.0e-35
Match length	70
% identity	100
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	237773
Seq. ID	uC-gsronu33B178a01b1
Method	BLASTX
NCBI GI	g3242708
BLAST score	471
E value	3.0e-47

Match length	172
% identity	53
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	237774
Seq. ID	uC-gsronu33B178a02b1
Method	BLASTX
NCBI GI	g114682
BLAST score	301
E value	3.0e-27
Match length	73
% identity	79
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No.	237775
Seq. ID	uC-gsronu33B178a10b1
Method	BLASTX
NCBI GI	g1084455
BLAST score	148
E value	9.0e-10
Match length	34
% identity	88
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	237776
Seq. ID	uC-gsronu33B178b09b1
Method	BLASTX
NCBI GI	g4263712
BLAST score	291
E value	3.0e-26
Match length	70
% identity	73
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	237777
Seq. ID	uC-gsronu33B178c04b1
Method	BLASTX
NCBI GI	g445612
BLAST score	227
E value	1.0e-18
Match length	46
% identity	98
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	237778
Seq. ID	uC-gsronu33B178c05b1
Method	BLASTX
NCBI GI	g3882151
BLAST score	181

E value	3.0e-13
Match length	131
% identity	27
NCBI Description	(AB018258) KIAA0715 protein [Homo sapiens]

Seq. No.	237779
Seq. ID	uC-gsronu33B178e03b1
Method	BLASTX
NCBI GI	g2507281
BLAST score	885
E value	1.0e-95
Match length	162
% identity	99
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	237780
Seq. ID	uC-gsronu33B178f04b1
Method	BLASTX
NCBI GI	g3006142
BLAST score	258
E value	3.0e-22
Match length	147
% identity	34
NCBI Description	(AL022299) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	237781
Seq. ID	uC-gsronu33B178f08b1
Method	BLASTX
NCBI GI	g4115731
BLAST score	192
E value	2.0e-14
Match length	98
% identity	43
NCBI Description	(AB017507) Apg12 [Homo sapiens]

Seq. No.	237782
Seq. ID	uC-gsronu33B178g05b1
Method	BLASTX
NCBI GI	g2062169
BLAST score	693
E value	3.0e-73
Match length	173
% identity	73
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	237783
Seq. ID	uC-gsronu33B178g10b1
Method	BLASTX
NCBI GI	g1518540
BLAST score	826
E value	8.0e-89
Match length	172
% identity	92
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	237784
Seq. ID	uC-gsronu33B178g11b1
Method	BLASTX
NCBI GI	g1737492
BLAST score	411
E value	4.0e-40
Match length	99
% identity	82
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	237785
Seq. ID	uC-gsronu33B178h10b1
Method	BLASTX
NCBI GI	g3757522
BLAST score	430
E value	2.0e-42
Match length	118
% identity	74
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	237786
Seq. ID	uC-gsronu33B179a01b1
Method	BLASTX
NCBI GI	g2655098
BLAST score	311
E value	2.0e-30
Match length	99
% identity	71
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	237787
Seq. ID	uC-gsronu33B179a09b1
Method	BLASTX
NCBI GI	g2967452
BLAST score	410
E value	4.0e-40
Match length	114
% identity	68
NCBI Description	(AB010882) hSNF2H [Homo sapiens] >gi_4507075_ref_NP_003592.1_pSMARCA5_ SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member

Seq. No.	237788
Seq. ID	uC-gsronu33B179a10b1
Method	BLASTX
NCBI GI	g2191130
BLAST score	139
E value	9.0e-09
Match length	78
% identity	42
NCBI Description	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]

Seq. No.	237789
Seq. ID	uC-gsronu33B179b10b1
Method	BLASTX
NCBI GI	g3341694

BLAST score	346
E value	1.0e-32
Match length	107
% identity	62
NCBI Description	(AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.	237790
Seq. ID	uC-gsronu33B179c01b1
Method	BLASTX
NCBI GI	g134944
BLAST score	537
E value	6.0e-55
Match length	115
% identity	87
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_100502_pir__A39173 acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) precursor - safflower >gi_167197 (M61109) stearoyl-acyl-carrier protein desaturase [Carthamus tinctorius]

Seq. No.	237791
Seq. ID	uC-gsronu33B179c08b1
Method	BLASTX
NCBI GI	g4544403
BLAST score	288
E value	9.0e-26
Match length	78
% identity	60
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]

Seq. No.	237792
Seq. ID	uC-gsronu33B179d02b1
Method	BLASTX
NCBI GI	g4185819
BLAST score	170
E value	5.0e-12
Match length	43
% identity	65
NCBI Description	(AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No.	237793
Seq. ID	uC-gsronu33B179d06b1
Method	BLASTX
NCBI GI	g3522945
BLAST score	132
E value	3.0e-11
Match length	91
% identity	41
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	237794
Seq. ID	uC-gsronu33B179e12b1
Method	BLASTX
NCBI GI	g1350548

BLAST score	184
E value	2.0e-13
Match length	92
% identity	39
NCBI Description	(L47609) heat shock-like protein [Picea glauca]

Seq. No.	237795
Seq. ID	uC-gsronu33B179g07b1
Method	BLASTX
NCBI GI	g2231312
BLAST score	213
E value	5.0e-17
Match length	47
% identity	81
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]

Seq. No.	237796
Seq. ID	uC-gsronu33B179h11b1
Method	BLASTX
NCBI GI	g2393767
BLAST score	137
E value	1.0e-08
Match length	35
% identity	74
NCBI Description	(U70621) phosphate-binding protein precursor [Erwinia carotovora subsp. carotovora]

Seq. No.	237797
Seq. ID	uC-gsronu33b023b01b1
Method	BLASTX
NCBI GI	g1737492
BLAST score	435
E value	4.0e-43
Match length	126
% identity	20
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	237798
Seq. ID	uC-gsronu33b023b05b1
Method	BLASTX
NCBI GI	g3915961
BLAST score	284
E value	5.0e-26
Match length	66
% identity	85
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	237799
Seq. ID	uC-gsronu33b023d04b1
Method	BLASTX
NCBI GI	g3617770
BLAST score	379
E value	1.0e-36
Match length	92

% identity	77
NCBI Description	(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	237800
Seq. ID	uC-gsronu33b023e02b1
Method	BLASTX
NCBI GI	g4455184
BLAST score	161
E value	5.0e-11
Match length	75
% identity	56
NCBI Description	(AL035521) extra-large G-protein-like [Arabidopsis thaliana]

Seq. No.	237801
Seq. ID	uC-gsronu33b023f05b1
Method	BLASTX
NCBI GI	g1076525
BLAST score	146
E value	2.0e-09
Match length	54
% identity	65
NCBI Description	dehydrin-related protein - garden pea >gi_18375_emb_CAA78515_ (Z14145) dehydrin-cognate [Pisum sativum]

Seq. No.	237802
Seq. ID	uC-gsronu33b023g01b1
Method	BLASTX
NCBI GI	g421843
BLAST score	371
E value	9.0e-36
Match length	101
% identity	69
NCBI Description	protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	237803
Seq. ID	uC-gsronu33b023h07b1
Method	BLASTX
NCBI GI	g1103318
BLAST score	242
E value	4.0e-23
Match length	69
% identity	80
NCBI Description	(X78818) casein kinase I [Arabidopsis thaliana] >gi_2244791_emb_CAB10213.1_ (Z97336) casein kinase I [Arabidopsis thaliana]

Seq. No.	237804
Seq. ID	uC-gsronu33b025c01b1
Method	BLASTX
NCBI GI	g1666173
BLAST score	144
E value	3.0e-09
Match length	32

% identity	91
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	237805
Seq. ID	uC-gsronu33b025d12b1
Method	BLASTX
NCBI GI	g1360088
BLAST score	316
E value	3.0e-29
Match length	78
% identity	71
NCBI Description	(X97947) Zn finger protein [Nicotiana tabacum]

Seq. No.	237806
Seq. ID	uC-gsronu33b025e04b1
Method	BLASTX
NCBI GI	g2062168
BLAST score	331
E value	5.0e-31
Match length	83
% identity	76
NCBI Description	(AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237807
Seq. ID	uC-gsronu33b025e08b1
Method	BLASTX
NCBI GI	g4220479
BLAST score	319
E value	1.0e-29
Match length	97
% identity	70
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	237808
Seq. ID	uC-gsronu33b025e10b1
Method	BLASTX
NCBI GI	g2623295
BLAST score	394
E value	2.0e-38
Match length	119
% identity	67
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237809
Seq. ID	uC-gsronu33b025e11b1
Method	BLASTX
NCBI GI	g2495230
BLAST score	531
E value	2.0e-54
Match length	115
% identity	89
NCBI Description	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >gi_1381086 (U49978) imidazoleglycerol-phosphate dehydratase [Pisum sativum]

Seq. No.	237810
Seq. ID	uC-gsronu33b025f07b1

Method	BLASTX
NCBI GI	g541951
BLAST score	445
E value	2.0e-44
Match length	113
% identity	79
NCBI Description	SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	237811
Seq. ID	uC-gsronu33b025f08b1
Method	BLASTX
NCBI GI	g129726
BLAST score	177
E value	8.0e-13
Match length	140
% identity	29
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55) >gi_68464_pir__ISBOSS protein disulfide-isomerase (EC 5.3.4.1) precursor - bovine >gi_163497 (M17596) PDI (E.C.5.3.4.1) [Bos taurus]

Seq. No.	237812
Seq. ID	uC-gsronu33b025f11b1
Method	BLASTX
NCBI GI	g541816
BLAST score	156
E value	8.0e-11
Match length	53
% identity	57
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	237813
Seq. ID	uC-gsronu33b025g06b1
Method	BLASTX
NCBI GI	g2208988
BLAST score	369
E value	2.0e-35
Match length	81
% identity	81
NCBI Description	(Y10117) signal recognition particle subunit 9 [Zea mays]

Seq. No.	237814
Seq. ID	uC-gsronu33b025h12b1
Method	BLASTX
NCBI GI	g3023832
BLAST score	355
E value	3.0e-34
Match length	78
% identity	82
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1 >gi_1835161_emb_CAB06618_ (Z84820) G protein beta subunit [Nicotiana tabacum]

Seq. No. 237815

Seq. ID	uC-gsronu33b112a02b1
Method	BLASTX
NCBI GI	g3831441
BLAST score	183
E value	2.0e-13
Match length	53
% identity	79
NCBI Description	(AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No.	237816
Seq. ID	uC-gsronu33b112b02b1
Method	BLASTX
NCBI GI	g3445207
BLAST score	172
E value	3.0e-12
Match length	121
% identity	34
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	237817
Seq. ID	uC-gsronu33b112c09b1
Method	BLASTX
NCBI GI	g4467145
BLAST score	195
E value	4.0e-15
Match length	41
% identity	88
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No.	237818
Seq. ID	uC-gsronu33b112e02b1
Method	BLASTX
NCBI GI	g3024017
BLAST score	462
E value	3.0e-46
Match length	100
% identity	91
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No.	237819
Seq. ID	uC-gsronu33b112e04b1
Method	BLASTX
NCBI GI	g2829899
BLAST score	240
E value	3.0e-20
Match length	87
% identity	51
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	237820
Seq. ID	uC-gsronu33b112e05b1
Method	BLASTX

NCBI GI	g3421090
BLAST score	424
E value	9.0e-42
Match length	88
% identity	92
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	237821
Seq. ID	uC-gsronu33b112f06b1
Method	BLASTX
NCBI GI	g1420887
BLAST score	156
E value	2.0e-10
Match length	92
% identity	35
NCBI Description	(U34334) non-specific lipid transfer-like protein [Phaseolus vulgaris]

Seq. No.	237822
Seq. ID	uC-gsronu33b112h05b1
Method	BLASTX
NCBI GI	g4490706
BLAST score	450
E value	9.0e-45
Match length	125
% identity	74
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	237823
Seq. ID	uC-gsronu33b112h08b1
Method	BLASTX
NCBI GI	g231536
BLAST score	183
E value	1.0e-13
Match length	90
% identity	51
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

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Doc 4 of 5 - 0054-0034

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Document 3 of 3

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Doc. 4 of 5

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Doc 5 of 5 - 00004

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Case 1:06-cv-00549-HHK Document 34-6 Filed 08/06/2007

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Case 4:05-cv-00037-YGR Document 925-34 Filed 09/26/14 Page 5 of 5

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US 9,598,703 B2

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Document 1 of 1

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WO 2007/146968 PCT/US2007/070959

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Case 3:06-cv-04505-SI Document 1-4 Filed 09/29/2006

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Case 4:09-cv-00037-Y Document 1-5 Filed 01/16/09 Page 34 of 50 PageID 34

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Case 4:07-cv-05944-JST Document 3204-9 Filed 06/04/15 Page 35002 of 35002

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Document 1 of 1 - Page 1 of 1000

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Document: 1-1 Page: 35026 of 35026

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Document 6 of 6

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Page 9 of 9 - 9/9/2008

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Document 1 of 3 Page 35351 of 35351

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Document 35373 of 35373

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Document 5 of 6

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Document 5 of 6

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Seq. No. 257951
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Seq. No. 257954
Seq. ID uC-gsronu33B162h03b2

Seq. No. 257955
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Seq. No. 257956
Seq. ID uC-gsronu33B163b03b2

Seq. No. 257957
Seq. ID uC-gsronu33B163b10b2

Seq. No. 257958
Seq. ID uC-gsronu33B163d07b2

Seq. No. 257959
Seq. ID uC-gsronu33B163f06b2

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Seq. No. 257963
Seq. ID uC-gsronu33B163h08b2

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Seq. ID uC-gsronu33B168e12b1

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Seq. ID uC-gsronu33B168g03b1

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Seq. ID uC-gsronu33B168g06b1

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Seq. ID uC-gsronu33B168h05b1

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Seq. ID uC-gsronu33B168h06b1

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Seq. ID uC-gsronu33B169a03b1

Seq. No. 258017
Seq. ID uC-gsronu33B169a04b1

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Seq. ID uC-gsronu33B169a06b1

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Seq. ID uC-gsronu33B169b06b1

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Seq. ID uC-gsronu33B169e03b1

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Seq. ID uC-gsronu33B169e04b1

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Seq. ID uC-gsronu33B169h02b1

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Seq. ID uC-gsronu33B169h04b1

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Seq. ID uC-gsronu33B170b02b1

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Seq. ID uC-gsronu33B170b11b1

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Seq. No. 258037
Seq. ID uC-gsronu33B170e04b1

Seq. No. 258038
Seq. ID uC-gsronu33B170e05b1

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Seq. ID uC-gsronu33B170f08b1

Seq. No. 258040
Seq. ID uC-gsronu33B170g12b1

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Seq. ID uC-gsronu33B170h03b1

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Seq. ID uC-gsronu33B170h05b1

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Seq. ID uC-gsronu33B171a11b1

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Seq. No. 258046
Seq. ID uC-gsronu33B171e05b1

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Seq. ID uC-gsronu33B172b01b1

Seq. No. 258048
Seq. ID uC-gsronu33B172b12b1

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Seq. ID uC-gsronu33B172d11b1

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Seq. ID uC-gsronu33B178c06b1

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Seq. ID uC-gsronu33B178d04b1

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Seq. ID uC-gsronu33B178d07b1

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Seq. ID uC-gsronu33B178e07b1

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Seq. ID uC-gsronu33B178e09b1

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Seq. ID uC-gsronu33B178f03b1

Seq. No. 258057
Seq. ID uC-gsronu33B178h02b1

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Seq. ID uC-gsronu33B178h05b1

Seq. No. 258059
Seq. ID uC-gsronu33B178h06b1

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Seq. ID uC-gsronu33B178h11b1

Seq. No. 258061
Seq. ID uC-gsronu33B179a02b1

Seq. No. 258062
Seq. ID uC-gsronu33B179c09b1

Seq. No. 258063
Seq. ID uC-gsronu33B179d05b1

Seq. No. 258064
Seq. ID uC-gsronu33B179e04b1

Seq. No. 258065
Seq. ID uC-gsronu33B179e05b1

Seq. No. 258066
Seq. ID uC-gsronu33B179f07b1

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Seq. ID uC-gsronu33B179g09b1

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Seq. ID uC-gsronu33b023d11b1

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Seq. ID uC-gsronu33b023e07b1

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Seq. ID uC-gsronu33b023e11b1

Seq. No. 258079
Seq. ID uC-gsronu33b023e12b1

Seq. No. 258080
Seq. ID uC-gsronu33b023f03b1

Seq. No. 258081
Seq. ID uC-gsronu33b023f12b1

Seq. No. 258082
Seq. ID uC-gsronu33b023h04b1

Seq. No. 258083
Seq. ID uC-gsronu33b023h08b1

Seq. No. 258084
Seq. ID uC-gsronu33b023h10b1

Seq. No. 258085
Seq. ID uC-gsronu33b025a10b1

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Seq. ID uC-gsronu33b025b02b1

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Seq. ID uC-gsronu33b025b03b1

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Seq. ID uC-gsronu33b025c06b1

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Seq. ID uC-gsronu33b025d01b1

Seq. No. 258092
Seq. ID uC-gsronu33b025d04b1

Seq. No. 258093
Seq. ID uC-gsronu33b025d07b1

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Seq. ID uC-gsronu33b025e06b1

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Seq. ID uC-gsronu33b025g05b1

Seq. No. 258096
Seq. ID uC-gsronu33b025h04b1

Seq. No. 258097
Seq. ID uC-gsronu33b025h05b1

Seq. No. 258098
Seq. ID uC-gsronu33b112a01b1

Seq. No. 258099
Seq. ID uC-gsronu33b112a06b1

Seq. No. 258100
Seq. ID uC-gsronu33b112a08b1

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Seq. No. 258101
Seq. ID uC-gsronu33b112b05b1

Seq. No. 258102
Seq. ID uC-gsronu33b112c01b1

Seq. No. 258103
Seq. ID uC-gsronu33b112c08b1

Seq. No. 258104
Seq. ID uC-gsronu33b112d04b1

Seq. No. 258105
Seq. ID uC-gsronu33b112f07b1

Seq. No. 258106
Seq. ID uC-gsronu33b112g05b1

Seq. No. 258107
Seq. ID uC-gsronu33b112h03b1

Seq. No. 258108
Seq. ID uC-gsronu33b112h09b1

Zea mays

Seq. No. 258109
Contig ID 0_1.R1011
5'-most EST >700042206.seq_FL
Method BLASTX
NCBI GI g1488255
BLAST score 729
E value 5.0e-77
Match length 215
% identity 64
NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574) ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No. 258110
Contig ID 1_1.R1011
5'-most EST LIB3078-038-Q1-K1-D7
Method BLASTX
NCBI GI g733456
BLAST score 1297
E value 1.0e-143
Match length 283
% identity 89
NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 258111
Contig ID 1_4.R1011
5'-most EST uC-zmflb73121g05a1
Method BLASTX
NCBI GI g733454

BLAST score	487
E value	5.0e-49
Match length	95
% identity	99
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	258112
Contig ID	1_7.R1011
5'-most EST	clt700041973.f1
Method	BLASTX
NCBI GI	g733454
BLAST score	696
E value	2.0e-73
Match length	158
% identity	85
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	258113
Contig ID	1_8.R1011
5'-most EST	fwa700098876.h1
Method	BLASTX
NCBI GI	g733454
BLAST score	182
E value	9.0e-14
Match length	38
% identity	100
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	258114
Contig ID	2_1.R1011
5'-most EST	700087981H1.FSEQ_FL
Method	BLASTX
NCBI GI	g1518540
BLAST score	2312
E value	0.0e+00
Match length	480
% identity	91
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	258115
Contig ID	2_2.R1011
5'-most EST	700336783SEQ_FL
Method	BLASTX
NCBI GI	g1518540
BLAST score	2007
E value	0.0e+00
Match length	428
% identity	92
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	258116
Contig ID	2_3.R1011
5'-most EST	LIB3150-075-P1-N1-E6
Method	BLASTX

NCBI GI	g1518540
BLAST score	2106
E value	0.0e+00
Match length	459
% identity	88
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	258117
Contig ID	2_5.R1011
5'-most EST	LIB3078-024-Q1-K1-B2
Method	BLASTX
NCBI GI	g1518540
BLAST score	529
E value	8.0e-54
Match length	107
% identity	89
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	258118
Contig ID	2_6.R1011
5'-most EST	xsy700211447.h1
Method	BLASTX
NCBI GI	g1518540
BLAST score	464
E value	2.0e-46
Match length	98
% identity	90
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	258119
Contig ID	2_7.R1011
5'-most EST	LIB3066-013-Q1-K1-A11
Method	BLASTX
NCBI GI	g1518540
BLAST score	504
E value	4.0e-57
Match length	136
% identity	85
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	258120
Contig ID	2_9.R1011
5'-most EST	LIB148-029-Q1-E1-C6
Method	BLASTX
NCBI GI	g1518540
BLAST score	159
E value	1.0e-10
Match length	44
% identity	77
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	258121
Contig ID	3_1.R1011
5'-most EST	xjt700093178.h1
Method	BLASTX
NCBI GI	g2827143
BLAST score	3361

E value	0.0e+00
Match length	816
% identity	77
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258122
Contig ID	3_2.R1011
5'-most EST	700210175H1.SEQ_FL
Method	BLASTX
NCBI GI	g2827143
BLAST score	2442
E value	0.0e+00
Match length	548
% identity	83
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258123
Contig ID	3_3.R1011
5'-most EST	LIB3062-041-Q1-K1-D12
Method	BLASTX
NCBI GI	g2827143
BLAST score	2193
E value	0.0e+00
Match length	506
% identity	81
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258124
Contig ID	3_4.R1011
5'-most EST	LIB3067-023-Q1-K1-E9
Method	BLASTX
NCBI GI	g2827143
BLAST score	504
E value	6.0e-51
Match length	100
% identity	91
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258125
Contig ID	3_5.R1011
5'-most EST	uC-zmflmo17310d04a1
Method	BLASTX
NCBI GI	g2827143
BLAST score	323
E value	7.0e-30
Match length	64
% identity	89
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258126
Contig ID	3_6.R1011
5'-most EST	uC-zmroteosinte099f03b2

Method	BLASTX
NCBI GI	g1706958
BLAST score	503
E value	7.0e-51
Match length	121
% identity	76
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	258127
Contig ID	4_1.R1011
5'-most EST	uC-zmflb73318a03b1

Seq. No.	258128
Contig ID	4_2.R1011
5'-most EST	pmx700086382.h1
Method	BLASTX
NCBI GI	g2117937
BLAST score	2008
E value	0.0e+00
Match length	471
% identity	83
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	258129
Contig ID	4_3.R1011
5'-most EST	uC-zmflm017207d05b1
Method	BLASTX
NCBI GI	g3107931
BLAST score	539
E value	1.0e-54
Match length	122
% identity	86
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	258130
Contig ID	6_1.R1011
5'-most EST	LIB36-009-Q1-E1-H8
Method	BLASTX
NCBI GI	g1666173
BLAST score	521
E value	1.0e-52
Match length	153
% identity	67
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	258131
Contig ID	6_2.R1011
5'-most EST	700167008_FL
Method	BLASTX
NCBI GI	g2982299
BLAST score	307
E value	9.0e-28
Match length	73
% identity	79
NCBI Description	(AF051234) transcription factor BTF3 homolog [Picea

mariana]

Seq. No.	258132
Contig ID	6_3.R1011
5'-most EST	xsy700212157.h1
Method	BLASTX
NCBI GI	g1666173
BLAST score	427
E value	8.0e-42
Match length	93
% identity	88
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No.	258133
Contig ID	6_5.R1011
5'-most EST	tfd700574011.h1

Seq. No.	258134
Contig ID	7_1.R1011
5'-most EST	uC-zmflb73076a04b2
Method	BLASTX
NCBI GI	g3924612
BLAST score	1483
E value	0.0e+00
Match length	443
% identity	76
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	258135
Contig ID	7_2.R1011
5'-most EST	wyr700236844.h1
Method	BLASTX
NCBI GI	g1694621
BLAST score	1551
E value	1.0e-173
Match length	461
% identity	63
NCBI Description	(D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No.	258136
Contig ID	7_3.R1011
5'-most EST	uC-zmflmo17099b11b1
Method	BLASTX
NCBI GI	g4504201
BLAST score	663
E value	7.0e-69
Match length	457
% identity	35
NCBI Description	general transcription factor IIH, polypeptide 4 (52kD subunit) >gi_1514597_emb_CAA68870_ (Y07595) transcription factor TFIIH [Homo sapiens]

Seq. No.	258137
Contig ID	7_4.R1011
5'-most EST	ymt700220389.h1

Seq. No.	258138
Contig ID	7_5.R1011
5'-most EST	uC-zmflb73305d04a1
Method	BLASTX
NCBI GI	g3924612
BLAST score	253
E value	1.0e-21
Match length	59
% identity	83
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	258139
Contig ID	7_7.R1011
5'-most EST	uC-zmflb73273h01a1

Seq. No.	258140
Contig ID	7_10.R1011
5'-most EST	uC-zmflmo17312g01b1
Method	BLASTX
NCBI GI	g3738297
BLAST score	604
E value	2.0e-62
Match length	322
% identity	23
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	258141
Contig ID	7_11.R1011
5'-most EST	uC-zmflb73040a07b1

Seq. No.	258142
Contig ID	7_12.R1011
5'-most EST	LIB143-001-Q1-E1-B9
Method	BLASTX
NCBI GI	g1351651
BLAST score	279
E value	2.0e-24
Match length	170
% identity	37
NCBI Description	HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I >gi_2130353_pir__S62553 hypothetical protein SPAC24B11.08c - fission yeast (Schizosaccharomyces pombe) >gi_1061296_emb_CAA91773_ (Z67757) unknown [Schizosaccharomyces pombe]

Seq. No.	258143
Contig ID	7_13.R1011
5'-most EST	xyt700343936.h1

Seq. No.	258144
Contig ID	7_14.R1011
5'-most EST	xsy700213359.h1
Method	BLASTX
NCBI GI	g3360289

BLAST score	291
E value	6.0e-26
Match length	69
% identity	75
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	258145
Contig ID	7_16.R1011
5'-most EST	LIB3115-017-P1-K1-D5
Method	BLASTX
NCBI GI	g4581114
BLAST score	302
E value	3.0e-27
Match length	79
% identity	72
NCBI Description	(AC005825) putative HesB-like protein;required for efficient nitrogen fixation in Cyanobacteria [Arabidopsis thaliana]

Seq. No.	258146
Contig ID	7_17.R1011
5'-most EST	uC-zmflmo17324f09a1
Method	BLASTN
NCBI GI	g12470
BLAST score	85
E value	1.0e-39
Match length	113
% identity	94
NCBI Description	Z.mays chloroplast rRNA-operon

Seq. No.	258147
Contig ID	7_19.R1011
5'-most EST	xmt700267948.h1

Seq. No.	258148
Contig ID	7_20.R1011
5'-most EST	ymt700219440.h1

Seq. No.	258149
Contig ID	7_21.R1011
5'-most EST	xsy700208548.h1
Method	BLASTX
NCBI GI	g3702326
BLAST score	252
E value	3.0e-38
Match length	138
% identity	65
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	258150
Contig ID	7_22.R1011
5'-most EST	LIB3078-023-Q1-K1-E2

Seq. No.	258151
Contig ID	7_23.R1011
5'-most EST	uC-zmflmo17150e02b1

Method	BLASTX
NCBI GI	g3149952
BLAST score	987
E value	1.0e-159
Match length	350
% identity	81
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	258152
Contig ID	7_24.R1011
5'-most EST	wty700165924.h1

Seq. No.	258153
Contig ID	7_25.R1011
5'-most EST	LIB3150-046-Q1-N1-G2
Method	BLASTX
NCBI GI	g4506233
BLAST score	384
E value	1.0e-36
Match length	257
% identity	37
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 >gi_1346766_sp_P48556_PSD8_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi_1362741_pir__S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 - human >gi_1037164_dbj_BAA07237_ (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi_3702282 (AC005789) PP31_HUMAN [Homo sapiens]

Seq. No.	258154
Contig ID	7_26.R1011
5'-most EST	uC-zmf1b73078h10b2

Seq. No.	258155
Contig ID	7_27.R1011
5'-most EST	qmh700026529.f1
Method	BLASTX
NCBI GI	g3738297
BLAST score	197
E value	6.0e-15
Match length	63
% identity	29
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	258156
Contig ID	7_28.R1011
5'-most EST	LIB3069-033-Q1-K1-H7

Seq. No.	258157
Contig ID	7_29.R1011
5'-most EST	LIB3067-038-Q1-K1-H1

Seq. No.	258158
Contig ID	7_30.R1011
5'-most EST	LIB3088-001-Q1-K1-E7

Seq. No.	258159

Contig ID 7_32.R1011
5'-most EST pmx700082907.h1

Seq. No. 258160
Contig ID 7_33.R1011
5'-most EST uC-zmflmo17128e03b1

Seq. No. 258161
Contig ID 7_34.R1011
5'-most EST xsy700208454.h1
Method BLASTX
NCBI GI g1351722
BLAST score 236
E value 3.0e-19
Match length 101
% identity 46
NCBI Description HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I >gi_1122371_emb_CAA92386_ (Z68198) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 258162
Contig ID 7_35.R1011
5'-most EST uC-zmflb73022h04b1
Method BLASTX
NCBI GI g3738297
BLAST score 425
E value 9.0e-42
Match length 143
% identity 28
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 258163
Contig ID 7_38.R1011
5'-most EST LIB3136-050-Q1-K1-F6
Method BLASTX
NCBI GI g4432857
BLAST score 273
E value 1.0e-23
Match length 103
% identity 48
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 258164
Contig ID 7_39.R1011
5'-most EST LIB3159-017-Q1-K1-G10
Method BLASTX
NCBI GI g1694621
BLAST score 642
E value 6.0e-67
Match length 174
% identity 72
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No. 258165
Contig ID 7_40.R1011
5'-most EST wty700167141.h1
Method BLASTX

NCBI GI	g3157941
BLAST score	281
E value	7.0e-25
Match length	101
% identity	49
NCBI Description	(AC002131) Contains similarity to hypothetical protein gb_U95973 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	258166
Contig ID	7_42.R1011
5'-most EST	uC-zmflmo17220f05b1

Seq. No.	258167
Contig ID	7_43.R1011
5'-most EST	LIB3150-035-Q1-N1-B12
Method	BLASTX
NCBI GI	g4506233
BLAST score	354
E value	4.0e-33
Match length	206
% identity	39
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 >gi_1346766_sp_P48556_PSD8_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi_1362741_pir__S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 - human >gi_1037164_dbj_BAA07237_ (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi_3702282 (AC005789) PP31_HUMAN [Homo sapiens]

Seq. No.	258168
Contig ID	7_44.R1011
5'-most EST	LIB189-023-Q1-E1-A9

Seq. No.	258169
Contig ID	7_45.R1011
5'-most EST	uC-zmroteosinte070b07b1
Method	BLASTX
NCBI GI	g1351722
BLAST score	162
E value	6.0e-11
Match length	175
% identity	30
NCBI Description	HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I >gi_1122371_emb_CAA92386_ (Z68198) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	258170
Contig ID	7_46.R1011
5'-most EST	LIB3067-025-Q1-K1-E6
Method	BLASTX
NCBI GI	g3702326
BLAST score	474
E value	3.0e-47
Match length	98
% identity	86
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 258171
Contig ID 7_47.R1011
5'-most EST uC-zmrob73004g08b1
Method BLASTX
NCBI GI g3738297
BLAST score 184
E value 1.0e-13
Match length 53
% identity 64
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 258172
Contig ID 7_48.R1011
5'-most EST uC-zmflmo17h11b1

Seq. No. 258173
Contig ID 7_49.R1011
5'-most EST LIB148-045-Q1-E1-D8

Seq. No. 258174
Contig ID 7_50.R1011
5'-most EST LIB3067-007-Q1-K1-G7

Seq. No. 258175
Contig ID 7_56.R1011
5'-most EST LIB143-042-Q1-E1-F6
Method BLASTX
NCBI GI g3149952
BLAST score 253
E value 1.0e-21
Match length 55
% identity 87
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

Seq. No. 258176
Contig ID 7_58.R1011
5'-most EST LIB3180-022-P2-M1-A10
Method BLASTX
NCBI GI g2494125
BLAST score 421
E value 8.0e-51
Match length 200
% identity 57
NCBI Description (AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb_D70895). [Arabidopsis thaliana]

Seq. No. 258177
Contig ID 7_59.R1011
5'-most EST LIB3150-100-P1-N1-A11

Seq. No. 258178
Contig ID 7_61.R1011
5'-most EST uC-zmflmo17179a04a1

Seq. No. 258179
Contig ID 7_62.R1011
5'-most EST tfd700575223.h1

Seq. No.	258180
Contig ID	7_63.R1011
5'-most EST	xjt700096568.h1
Method	BLASTX
NCBI GI	g3149952
BLAST score	340
E value	6.0e-32
Match length	107
% identity	62
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	258181
Contig ID	7_66.R1011
5'-most EST	nbm700476596.h1

Seq. No.	258182
Contig ID	7_68.R1011
5'-most EST	pwr700448842.h1

Seq. No.	258183
Contig ID	7_76.R1011
5'-most EST	pmx700091114.h1

Seq. No.	258184
Contig ID	9_1.R1011
5'-most EST	700193495_FL
Method	BLASTX
NCBI GI	g862644
BLAST score	246
E value	2.0e-20
Match length	133
% identity	47
NCBI Description	(U20184) MADS-box protein AGL14 [Arabidopsis thaliana]

Seq. No.	258185
Contig ID	9_3.R1011
5'-most EST	uC-zmflmo17066b05b1
Method	BLASTX
NCBI GI	g3759184
BLAST score	166
E value	2.0e-11
Match length	77
% identity	39
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	258186
Contig ID	9_4.R1011
5'-most EST	LIB3136-060-Q1-K1-E4
Method	BLASTX
NCBI GI	g3759184
BLAST score	663
E value	5.0e-85
Match length	284
% identity	56
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	258187
Contig ID	9_5.R1011
5'-most EST	hvj700621362.h1
Method	BLASTN
NCBI GI	g169818
BLAST score	100
E value	1.0e-48
Match length	124
% identity	95
NCBI Description	Rice 25S ribosomal RNA gene

Seq. No.	258188
Contig ID	9_6.R1011
5'-most EST	uC-zmflmo17060g07a1
Method	BLASTX
NCBI GI	g3759184
BLAST score	305
E value	7.0e-28
Match length	74
% identity	74
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	258189
Contig ID	9_7.R1011
5'-most EST	LIB3088-008-Q1-K1-D6

Seq. No.	258190
Contig ID	9_8.R1011
5'-most EST	LIB3066-033-Q1-K1-F10

Seq. No.	258191
Contig ID	9_9.R1011
5'-most EST	uC-zmflb73110b09a1
Method	BLASTN
NCBI GI	g169818
BLAST score	335
E value	0.0e+00
Match length	391
% identity	96
NCBI Description	Rice 25S ribosomal RNA gene

Seq. No.	258192
Contig ID	9_10.R1011
5'-most EST	LIB3067-053-Q1-K1-D10

Seq. No.	258193
Contig ID	9_11.R1011
5'-most EST	xsy700209434.h1

Seq. No.	258194
Contig ID	10_1.R1011
5'-most EST	wyr700238151.h1
Method	BLASTX
NCBI GI	g1351222
BLAST score	1376
E value	1.0e-153
Match length	312

09604705.700001

% identity	84
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945087 (U31097) transcription factor TFIIB [Glycine max]

Seq. No.	258195
Contig ID	10_2.R1011
5'-most EST	LIB3062-045-Q1-K1-B11
Method	BLASTX
NCBI GI	g1351222
BLAST score	207
E value	2.0e-16
Match length	47
% identity	83
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945087 (U31097) transcription factor TFIIB [Glycine max]

Seq. No.	258196
Contig ID	10_3.R1011
5'-most EST	hvj700618843.h1
Method	BLASTX
NCBI GI	g1351222
BLAST score	216
E value	1.0e-17
Match length	45
% identity	80
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945087 (U31097) transcription factor TFIIB [Glycine max]

Seq. No.	258197
Contig ID	11_1.R1011
5'-most EST	700201723_FL

Seq. No.	258198
Contig ID	12_1.R1011
5'-most EST	700206101H1.SEQ_FL
Method	BLASTX
NCBI GI	g2924781
BLAST score	489
E value	4.0e-49
Match length	175
% identity	54
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	258199
Contig ID	13_1.R1011
5'-most EST	ntr700071667.h1
Method	BLASTX
NCBI GI	g1362086
BLAST score	3447
E value	0.0e+00
Match length	766
% identity	87
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine

	S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]
Seq. No.	258200
Contig ID	13_2.R1011
5'-most EST	LIB3067-001-Q1-K1-C6
Method	BLASTX
NCBI GI	g1362086
BLAST score	858
E value	3.0e-92
Match length	194
% identity	85
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]
Seq. No.	258201
Contig ID	13_3.R1011
5'-most EST	xsy700208732.h1
Method	BLASTX
NCBI GI	g1814403
BLAST score	593
E value	3.0e-67
Match length	150
% identity	81
NCBI Description	(U84889) methionine synthase [Mesembryanthemum crystallinum]
Seq. No.	258202
Contig ID	13_4.R1011
5'-most EST	LIB143-021-Q1-E1-F9
Seq. No.	258203
Contig ID	13_8.R1011
5'-most EST	ymt700224308.h1
Method	BLASTX
NCBI GI	g1814403
BLAST score	713
E value	2.0e-75
Match length	151
% identity	87
NCBI Description	(U84889) methionine synthase [Mesembryanthemum crystallinum]
Seq. No.	258204
Contig ID	13_17.R1011
5'-most EST	cyk700051461.f1
Method	BLASTX
NCBI GI	g2738248
BLAST score	464
E value	3.0e-46
Match length	198

% identity	54
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	258205
Contig ID	13_21.R1011
5'-most EST	LIB143-027-Q1-E1-H3
Method	BLASTX
NCBI GI	g1814403
BLAST score	339
E value	4.0e-38
Match length	83
% identity	90
NCBI Description	(U84889) methionine synthase [Mesembryanthemum crystallinum]

Seq. No.	258206
Contig ID	14_1.R1011
5'-most EST	700209062H1.SEQ_FL
Method	BLASTX
NCBI GI	g2117937
BLAST score	2106
E value	0.0e+00
Match length	473
% identity	87
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	258207
Contig ID	14_2.R1011
5'-most EST	uC-zmf1b73185f09b1
Method	BLASTX
NCBI GI	g2117937
BLAST score	2106
E value	0.0e+00
Match length	473
% identity	87
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	258208
Contig ID	14_3.R1011
5'-most EST	LIB3150-039-Q1-N1-C5
Method	BLASTX
NCBI GI	g2117937
BLAST score	1413
E value	1.0e-157
Match length	303
% identity	90
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	258209
Contig ID	14_4.R1011

5'-most EST	uC-zmroteosinte102h03b2
Method	BLASTX
NCBI GI	g136739
BLAST score	610
E value	3.0e-63
Match length	138
% identity	85
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	258210
Contig ID	14_6.R1011
5'-most EST	pwr700449014.h1
Method	BLASTX
NCBI GI	g2245108
BLAST score	513
E value	1.0e-51
Match length	139
% identity	63
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	258211
Contig ID	14_7.R1011
5'-most EST	uC-zmroteosinte001a12b1
Method	BLASTX
NCBI GI	g136739
BLAST score	231
E value	7.0e-19
Match length	67
% identity	66
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	258212
Contig ID	14_17.R1011
5'-most EST	uC-zmflmo17215h07b1
Method	BLASTX
NCBI GI	g2117937
BLAST score	437
E value	8.0e-61
Match length	133
% identity	89
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	258213
Contig ID	16_1.R1011
5'-most EST	700219515_FL
Method	BLASTX
NCBI GI	g4038471

BLAST score	401
E value	1.0e-38
Match length	86
% identity	88
NCBI Description	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No.	258214
Contig ID	16_2.R1011
5'-most EST	uC-zmflb73219a01b2
Method	BLASTX
NCBI GI	g4038471
BLAST score	283
E value	6.0e-25
Match length	51
% identity	100
NCBI Description	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No.	258215
Contig ID	16_3.R1011
5'-most EST	LIB3116-006-Q1-K1-D10
Method	BLASTX
NCBI GI	g4038471
BLAST score	401
E value	5.0e-39
Match length	86
% identity	88
NCBI Description	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No.	258216
Contig ID	17_1.R1011
5'-most EST	700221310_FL
Method	BLASTX
NCBI GI	g1346790
BLAST score	780
E value	1.0e-82
Match length	443
% identity	42
NCBI Description	PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHA) >gi_507220 (L21991) homeodomain protein [Arabidopsis thaliana] >gi_2501810 (U48864) PRHA [Arabidopsis thaliana]

Seq. No.	258217
Contig ID	18_1.R1011
5'-most EST	uC-zmroteosinte075d04b1
Method	BLASTX
NCBI GI	g3264767
BLAST score	385
E value	1.0e-36
Match length	247
% identity	39
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	258218
Contig ID	18_2.R1011
5'-most EST	uC-zmflmo17282g03b1
Method	BLASTN
NCBI GI	g2443456

BLAST score 36
E value 1.0e-10
Match length 88
% identity 85
NCBI Description Oryza sativa ethylene responsive element binding protein (Os-EREBP1) mRNA, complete cds

Seq. No. 258219
Contig ID 18_3.R1011
5'-most EST LIB189-022-Q1-E1-B5
Method BLASTX
NCBI GI g3264767
BLAST score 221
E value 1.0e-17
Match length 138
% identity 42
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 258220
Contig ID 18_5.R1011
5'-most EST dyk700104338.h1
Method BLASTX
NCBI GI g3264767
BLAST score 199
E value 3.0e-15
Match length 146
% identity 39
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 258221
Contig ID 19_1.R1011
5'-most EST CPR21928:2F700212293H1.seq_FL
Method BLASTX
NCBI GI g2827141
BLAST score 3739
E value 0.0e+00
Match length 963
% identity 71
NCBI Description (AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 258222
Contig ID 19_2.R1011
5'-most EST cyk700050280.f1
Method BLASTX
NCBI GI g2827141
BLAST score 1932
E value 0.0e+00
Match length 694
% identity 71
NCBI Description (AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 258223
Contig ID 19_3.R1011
5'-most EST pmx700088647.h1
Method BLASTX

NCBI GI	g2827141
BLAST score	3357
E value	0.0e+00
Match length	825
% identity	74
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258224
Contig ID	19_4.R1011
5'-most EST	LIB3158-010-Q1-K1-B4

Seq. No.	258225
Contig ID	19_6.R1011
5'-most EST	ntr700076906.h1
Method	BLASTX
NCBI GI	g2252631
BLAST score	199
E value	6.0e-15
Match length	120
% identity	46
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	258226
Contig ID	19_7.R1011
5'-most EST	uC-zmflmo17158h12b1
Method	BLASTX
NCBI GI	g2827143
BLAST score	737
E value	3.0e-78
Match length	180
% identity	73
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258227
Contig ID	19_8.R1011
5'-most EST	xsy700214883.h1
Method	BLASTX
NCBI GI	g1706958
BLAST score	177
E value	1.0e-12
Match length	69
% identity	49
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	258228
Contig ID	19_10.R1011
5'-most EST	uC-zmflmo17025d07a1
Method	BLASTX
NCBI GI	g3287270
BLAST score	148
E value	2.0e-09
Match length	43
% identity	63
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	258229
Contig ID	19_11.R1011
5'-most EST	uC-zmflb73140a09b1

Seq. No.	258230
Contig ID	19_12.R1011
5'-most EST	uC-zmflb73214g05b1
Method	BLASTX
NCBI GI	g2827141
BLAST score	1631
E value	0.0e+00
Match length	416
% identity	70
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258231
Contig ID	19_13.R1011
5'-most EST	uC-zmflMo17093d02b1
Method	BLASTX
NCBI GI	g2827141
BLAST score	152
E value	1.0e-09
Match length	33
% identity	76
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258232
Contig ID	19_15.R1011
5'-most EST	LIB3069-022-Q1-K1-B7

Seq. No.	258233
Contig ID	19_17.R1011
5'-most EST	LIB3067-050-Q1-K1-G2

Seq. No.	258234
Contig ID	19_20.R1011
5'-most EST	LIB3136-017-Q1-K1-F6

Seq. No.	258235
Contig ID	19_24.R1011
5'-most EST	xsy700210709.h1
Method	BLASTX
NCBI GI	g1706958
BLAST score	447
E value	2.0e-44
Match length	113
% identity	70
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	258236
Contig ID	22_1.R1011
5'-most EST	700350212.SEQ_FL
Method	BLASTX
NCBI GI	g1709205
BLAST score	312

E value	1.0e-28
Match length	82
% identity	70
NCBI Description	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL MONOPHOSPHATASE 3) >gi_1098971 (U39059) myo-inositol monophosphatase 3 [Lycopersicon esculentum]

Seq. No.	258237
Contig ID	23_1.R1011
5'-most EST	uC-zmflb73125f11a1

Seq. No.	258238
Contig ID	23_2.R1011
5'-most EST	LIB3069-011-Q1-K1-E7

Seq. No.	258239
Contig ID	24_1.R1011
5'-most EST	uC-zmflb73156c09b1
Method	BLASTX
NCBI GI	g2827139
BLAST score	3903
E value	0.0e+00
Match length	856
% identity	82
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	258240
Contig ID	24_2.R1011
5'-most EST	LIB3137-023-Q1-K1-B7
Method	BLASTX
NCBI GI	g1706956
BLAST score	1926
E value	0.0e+00
Match length	429
% identity	83
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	258241
Contig ID	24_3.R1011
5'-most EST	uC-zmroteosinte058e03b2
Method	BLASTX
NCBI GI	g2827143
BLAST score	404
E value	4.0e-39
Match length	84
% identity	87
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	258242
Contig ID	24_4.R1011
5'-most EST	xjt700092688.h1
Method	BLASTX
NCBI GI	g2781433

BLAST score 628
E value 4.0e-65
Match length 143
% identity 81
NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit [Oryza sativa subsp. japonica]

Seq. No. 258243
Contig ID 24_5.R1011
5'-most EST LIB3067-053-Q1-K1-C8
Method BLASTX
NCBI GI g1706958
BLAST score 310
E value 3.0e-28
Match length 75
% identity 77
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 258244
Contig ID 25_1.R1011
5'-most EST LIB148-047-Q1-E1-D5
Method BLASTX
NCBI GI g2150002
BLAST score 931
E value 1.0e-100
Match length 203
% identity 79
NCBI Description (AF000940) ribonuclease [Hordeum vulgare]

Seq. No. 258245
Contig ID 26_1.R1011
5'-most EST LIB148-038-Q1-E1-H7
Method BLASTX
NCBI GI g1864024
BLAST score 222
E value 1.0e-26
Match length 79
% identity 84
NCBI Description (U35683) calcium-binding pollen allergen [Cynodon dactylon] >gi_1871507_emb_CAA62634_ (X91256) calcium-binding pollen allergen [Cynodon dactylon]

Seq. No. 258246
Contig ID 26_3.R1011
5'-most EST LIB3066-048-Q1-K1-D2

Seq. No. 258247
Contig ID 26_4.R1011
5'-most EST LIB3075-010-Q1-K1-C2
Method BLASTX
NCBI GI g1864024
BLAST score 185
E value 7.0e-23
Match length 72
% identity 83
NCBI Description (U35683) calcium-binding pollen allergen [Cynodon dactylon] >gi_1871507_emb_CAA62634_ (X91256) calcium-binding pollen

allergen [Cynodon dactylon]

Seq. No.	258248
Contig ID	26_5.R1011
5'-most EST	uC-zmflb73125e09a1
Method	BLASTX
NCBI GI	g1504052
BLAST score	2382
E value	0.0e+00
Match length	471
% identity	98
NCBI Description	(D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No.	258249
Contig ID	26_6.R1011
5'-most EST	LIB3059-034-Q1-K1-C5
Method	BLASTN
NCBI GI	g4160401
BLAST score	155
E value	2.0e-81
Match length	303
% identity	88
NCBI Description	Zea mays eIF-5 gene, exons 1-2

Seq. No.	258250
Contig ID	26_7.R1011
5'-most EST	LIB148-049-Q1-E1-G3
Method	BLASTN
NCBI GI	g4160401
BLAST score	109
E value	3.0e-54
Match length	184
% identity	90
NCBI Description	Zea mays eIF-5 gene, exons 1-2

Seq. No.	258251
Contig ID	26_10.R1011
5'-most EST	LIB3075-034-Q1-K1-C2
Method	BLASTX
NCBI GI	g1864024
BLAST score	373
E value	9.0e-36
Match length	80
% identity	90
NCBI Description	(U35683) calcium-binding pollen allergen [Cynodon dactylon] >gi_1871507_emb_CAA62634_ (X91256) calcium-binding pollen allergen [Cynodon dactylon]

Seq. No.	258252
Contig ID	26_11.R1011
5'-most EST	uC-zmroteosinte099c10b2
Method	BLASTX
NCBI GI	g1504052
BLAST score	507
E value	2.0e-51
Match length	96
% identity	100

NCBI Description	(D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No.	258253
Contig ID	26_16.R1011
5'-most EST	uC-zmflmo17405a02a1
Method	BLASTN
NCBI GI	g4160401
BLAST score	95
E value	7.0e-46
Match length	146
% identity	92
NCBI Description	Zea mays eIF-5 gene, exons 1-2

Seq. No.	258254
Contig ID	26_17.R1011
5'-most EST	vux700157212.h1
Method	BLASTX
NCBI GI	g2795876
BLAST score	345
E value	1.0e-32
Match length	130
% identity	54
NCBI Description	(AF020726) phosphoglucomutase [Tetrahymena thermophila]

Seq. No.	258255
Contig ID	27_1.R1011
5'-most EST	LIB148-004-Q1-E1-D9
Method	BLASTN
NCBI GI	g507770
BLAST score	53
E value	4.0e-20
Match length	174
% identity	89
NCBI Description	Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete cds

Seq. No.	258256
Contig ID	27_2.R1011
5'-most EST	uC-zmflmo17035d05a1
Method	BLASTX
NCBI GI	g130582
BLAST score	186
E value	7.0e-14
Match length	110
% identity	34
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi_100342_pir__S04273 hypothetical protein - common tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana tabacum]

Seq. No.	258257
Contig ID	27_3.R1011
5'-most EST	LIB3066-043-Q1-K1-G10
Method	BLASTX
NCBI GI	g3702317
BLAST score	150

E value	2.0e-09
Match length	34
% identity	85
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana] >gi_4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	258258
Contig ID	28_1.R1011
5'-most EST	CPR10368consensus_FL
Method	BLASTX
NCBI GI	g121277
BLAST score	1430
E value	1.0e-159
Match length	349
% identity	83
NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max] >gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin [Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]

Seq. No.	258259
Contig ID	29_1.R1011
5'-most EST	CPR11053consensus_FL
Method	BLASTX
NCBI GI	g20559
BLAST score	1342
E value	1.0e-149
Match length	347
% identity	93
NCBI Description	(X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]

Seq. No.	258260
Contig ID	29_2.R1011
5'-most EST	uC-zmf1b73199a09b1
Method	BLASTX
NCBI GI	g123650
BLAST score	1814
E value	0.0e+00
Match length	462
% identity	78
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat shock protein 70 (clone pMON9743) - garden petunia >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida]

Seq. No.	258261
Contig ID	29_3.R1011
5'-most EST	LIB148-044-Q1-E1-F12
Method	BLASTX
NCBI GI	g2827002
BLAST score	1071

E value	1.0e-117
Match length	260
% identity	82
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	258262
Contig ID	30_1.R1011
5'-most EST	CPR11054consensus_FL
Method	BLASTX
NCBI GI	g2827002
BLAST score	1130
E value	1.0e-123
Match length	294
% identity	76
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	258263
Contig ID	30_2.R1011
5'-most EST	LIB3150-017-Q1-N1-C9
Method	BLASTX
NCBI GI	g1076746
BLAST score	1922
E value	0.0e+00
Match length	459
% identity	83
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	258264
Contig ID	30_3.R1011
5'-most EST	uC-zmf1b73050d09b1
Method	BLASTX
NCBI GI	g3264596
BLAST score	993
E value	1.0e-108
Match length	249
% identity	80
NCBI Description	(AF057183) putative tonoplast aquaporin [Zea mays]

Seq. No.	258265
Contig ID	30_4.R1011
5'-most EST	uC-zmroteosinte119d06b2
Method	BLASTX
NCBI GI	g861170
BLAST score	423
E value	2.0e-41
Match length	108
% identity	78
NCBI Description	(X03697) heat shock protein 70 [Zea mays]

Seq. No.	258266
Contig ID	30_5.R1011
5'-most EST	tzu700206071.h1
Method	BLASTX
NCBI GI	g1549339
BLAST score	374

E value	9.0e-36
Match length	81
% identity	89
NCBI Description	(U58207) aquaporin homologue [Allium cepa]

Seq. No.	258267
Contig ID	30_6.R1011
5'-most EST	uC-zmflmo17021h05b1
Method	BLASTX
NCBI GI	g2827002
BLAST score	1150
E value	1.0e-126
Match length	234
% identity	95
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	258268
Contig ID	30_7.R1011
5'-most EST	uC-zmflb73378e05a2
Method	BLASTX
NCBI GI	g3264596
BLAST score	935
E value	1.0e-101
Match length	261
% identity	74
NCBI Description	(AF057183) putative tonoplast aquaporin [Zea mays]

Seq. No.	258269
Contig ID	30_8.R1011
5'-most EST	uC-zmroteosinte066a07b1
Method	BLASTX
NCBI GI	g3264596
BLAST score	474
E value	2.0e-47
Match length	132
% identity	73
NCBI Description	(AF057183) putative tonoplast aquaporin [Zea mays]

Seq. No.	258270
Contig ID	30_9.R1011
5'-most EST	LIB143-030-Q1-E1-A12
Method	BLASTX
NCBI GI	g3128175
BLAST score	147
E value	5.0e-09
Match length	48
% identity	60
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	258271
Contig ID	30_10.R1011
5'-most EST	uC-zmflb73137b08a1
Method	BLASTN
NCBI GI	g3264595
BLAST score	66
E value	1.0e-28
Match length	136

% identity	88
NCBI Description	Zea mays putative tonoplast aquaporin mRNA, complete cds

Seq. No.	258272
Contig ID	30_13.R1011
5'-most EST	LIB3069-010-Q1-K1-B1

Seq. No.	258273
Contig ID	30_15.R1011
5'-most EST	ntr700072741.h1
Method	BLASTX
NCBI GI	g3264596
BLAST score	438
E value	2.0e-55
Match length	127
% identity	93
NCBI Description	(AF057183) putative tonoplast aquaporin [Zea mays]

Seq. No.	258274
Contig ID	30_16.R1011
5'-most EST	dyk700106039.h1
Method	BLASTX
NCBI GI	g461929
BLAST score	272
E value	4.0e-24
Match length	83
% identity	67
NCBI Description	PROBABLE TONOPLAST INTRINSIC PROTEIN DIP >gi_1076688_pir__S51781 integral membrane protein - garden snapdragon >gi_414088_emb_CAA49854_ (X70417) integral membrane protein [Antirrhinum majus]

Seq. No.	258275
Contig ID	30_17.R1011
5'-most EST	LIB3136-001-P1-K1-F3
Method	BLASTX
NCBI GI	g3128176
BLAST score	317
E value	5.0e-29
Match length	106
% identity	57
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	258276
Contig ID	30_18.R1011
5'-most EST	uC-zmflm017084c07b1
Method	BLASTX
NCBI GI	g224970
BLAST score	262
E value	5.0e-23
Match length	83
% identity	75
NCBI Description	heat shock protein hsp70 [Zea mays]

Seq. No.	258277
Contig ID	30_21.R1011
5'-most EST	uC-zmflb73372b07a1

Method	BLASTN
NCBI GI	g22342
BLAST score	125
E value	5.0e-64
Match length	157
% identity	95
NCBI Description	Maize gene for heat shock protein 70 exon 2 and 3'-UT (hsp70; clone pMON 9502)

Seq. No.	258278
Contig ID	31_1.R1011
5'-most EST	CPR1375_700047754_FL
Method	BLASTX
NCBI GI	g3935138
BLAST score	777
E value	2.0e-82
Match length	340
% identity	43
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	258279
Contig ID	32_1.R1011
5'-most EST	uC-zmroteosinte069b07b1
Method	BLASTX
NCBI GI	g3135256
BLAST score	440
E value	5.0e-43
Match length	299
% identity	35
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.	258280
Contig ID	33_1.R1011
5'-most EST	CPR1377_700085012_FL
Method	BLASTX
NCBI GI	g3540206
BLAST score	504
E value	2.0e-50
Match length	244
% identity	41
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	258281
Contig ID	34_1.R1011
5'-most EST	LIB3076-055-Q1-K1-D7
Method	BLASTX
NCBI GI	g3236235
BLAST score	892
E value	1.0e-103
Match length	455
% identity	44
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana] >gi_4056501 (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	258282
Contig ID	36_1.R1011

5'-most EST	LIB3066-008-Q1-K1-F10
Method	BLASTX
NCBI GI	g3935138
BLAST score	410
E value	3.0e-39
Match length	161
% identity	48
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	258283
Contig ID	37_1.R1011
5'-most EST	uC-zmrob73019b04b1
Method	BLASTX
NCBI GI	g4510418
BLAST score	1288
E value	1.0e-142
Match length	688
% identity	43
NCBI Description	(AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No.	258284
Contig ID	39_1.R1011
5'-most EST	CPR1387_700441447_FL

Seq. No.	258285
Contig ID	39_2.R1011
5'-most EST	LIB84-012-Q1-E12-D4

Seq. No.	258286
Contig ID	39_3.R1011
5'-most EST	uC-zmflmo17100h09b1

Seq. No.	258287
Contig ID	40_1.R1011
5'-most EST	CPR1431FL_700166721_FL
Method	BLASTX
NCBI GI	g4539677
BLAST score	1880
E value	0.0e+00
Match length	404
% identity	90
NCBI Description	(AF061282) patatin-like protein [Sorghum bicolor]

Seq. No.	258288
Contig ID	40_2.R1011
5'-most EST	CPR1430consensus_FL
Method	BLASTX
NCBI GI	g4539677
BLAST score	1886
E value	0.0e+00
Match length	409
% identity	90
NCBI Description	(AF061282) patatin-like protein [Sorghum bicolor]

Seq. No.	258289
Contig ID	45_2.R1011
5'-most EST	LIB148-012-Q1-E1-F6

Method	BLASTX
NCBI GI	g729944
BLAST score	1028
E value	1.0e-112
Match length	191
% identity	97
NCBI Description	POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea mI [Zea mays]

Seq. No.	258290
Contig ID	45_4.R1011
5'-most EST	LIB3075-032-Q1-K1-G1
Method	BLASTX
NCBI GI	g729944
BLAST score	297
E value	7.0e-27
Match length	57
% identity	96
NCBI Description	POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea mI [Zea mays]

Seq. No.	258291
Contig ID	45_10.R1011
5'-most EST	LIB3075-029-Q1-K1-G3
Method	BLASTX
NCBI GI	g729944
BLAST score	891
E value	4.0e-96
Match length	181
% identity	92
NCBI Description	POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir__JC1524 major allergen mI protein - maize >gi_293902 (L14271) Zea mI [Zea mays]

Seq. No.	258292
Contig ID	46_1.R1011
5'-most EST	gct701176810.h1
Method	BLASTX
NCBI GI	g563235
BLAST score	521
E value	7.0e-53
Match length	181
% identity	53
NCBI Description	(U15964) xyloglucan endo-transglycosylase homolog; similar to Triticum aestivum endo-xyloglucan transferase, PIR Accession Number E49539 [Zea mays] >gi_563927 (U15781) xyloglucan endo-transglycosylase homolog [Zea mays] >gi_1097378_prf__2113418A xyloglucan endotransglycosylase homolog [Zea mays]

Seq. No.	258293
Contig ID	47_1.R1011
5'-most EST	CPR22012consensus_FL
Method	BLASTX
NCBI GI	g1890577

BLAST score 639
E value 1.0e-66
Match length 172
% identity 67
NCBI Description (X93175) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No. 258294
Contig ID 48_1.R1011
5'-most EST CPR22042consensus_FL
Method BLASTX
NCBI GI g2960364
BLAST score 890
E value 8.0e-96
Match length 320
% identity 52
NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No. 258295
Contig ID 49_1.R1011
5'-most EST pwr700450831.h1
Method BLASTX
NCBI GI g3603401
BLAST score 967
E value 1.0e-105
Match length 341
% identity 54
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 258296
Contig ID 49_3.R1011
5'-most EST uC-zmf1b73092g10b2
Method BLASTX
NCBI GI g1168727
BLAST score 149
E value 2.0e-09
Match length 51
% identity 53
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol dehydrogenase [Aralia cordata] >gi_745086_prf__2015401A cinnamoyl alcohol dehydrogenase [Aralia cordata]

Seq. No. 258297
Contig ID 50_1.R1011
5'-most EST CPR22074consensus_FL
Method BLASTX
NCBI GI g1724110
BLAST score 975
E value 1.0e-106
Match length 342
% identity 53
NCBI Description (U79770) cinnamyl-alcohol dehydrogenase Eli3 [Mesembryanthemum crystallinum]

Seq. No. 258298

Contig ID	51_1.R1011
5'-most EST	uC-zmflb73040b09b1
Method	BLASTX
NCBI GI	g82496
BLAST score	3032
E value	0.0e+00
Match length	701
% identity	85
NCBI Description	phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

Seq. No.	258299
Contig ID	51_2.R1011
5'-most EST	qmh700029234.f1
Method	BLASTX
NCBI GI	g1944573
BLAST score	777
E value	1.0e-82
Match length	210
% identity	71
NCBI Description	(Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No.	258300
Contig ID	51_3.R1011
5'-most EST	uC-zmflb73079b05b2
Method	BLASTX
NCBI GI	g3024363
BLAST score	1169
E value	1.0e-128
Match length	306
% identity	75
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi_1483610_emb_CAA68036_ (X99705) phenylalanine ammonia-lyase [Triticum aestivum]

Seq. No.	258301
Contig ID	51_4.R1011
5'-most EST	uC-zmflb73057a03b1
Method	BLASTX
NCBI GI	g1944573
BLAST score	649
E value	9.0e-68
Match length	162
% identity	75
NCBI Description	(Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No.	258302
Contig ID	51_5.R1011
5'-most EST	LIB3067-045-Q1-K1-A6
Method	BLASTX
NCBI GI	g168570
BLAST score	267
E value	3.0e-23
Match length	49
% identity	100
NCBI Description	(M95077) phenylalanine ammonia-lyase [Zea mays]

Seq. No.	258303
Contig ID	51_6.R1011

5'-most EST	LIB3062-027-Q1-K1-D8
Method	BLASTX
NCBI GI	g3024363
BLAST score	709
E value	4.0e-90
Match length	211
% identity	79
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi_1483610_emb_CAA68036_ (X99705) phenylalanine ammonia-lyase [Triticum aestivum]

Seq. No.	258304
Contig ID	51_16.R1011
5'-most EST	uC-zmflb73206f04b1
Method	BLASTX
NCBI GI	g82496
BLAST score	858
E value	3.0e-92
Match length	177
% identity	94
NCBI Description	phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

Seq. No.	258305
Contig ID	52_1.R1011
5'-most EST	CPR22357consensus_FL
Method	BLASTX
NCBI GI	g99699
BLAST score	1740
E value	0.0e+00
Match length	356
% identity	94
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgsr1) - Arabidopsis thaliana

Seq. No.	258306
Contig ID	54_1.R1011
5'-most EST	LIB189-024-Q1-E1-B5
Method	BLASTX
NCBI GI	g3913018
BLAST score	1819
E value	0.0e+00
Match length	388
% identity	92
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	258307
Contig ID	54_2.R1011
5'-most EST	LIB3067-031-Q1-K1-B11
Method	BLASTX
NCBI GI	g2497748
BLAST score	261
E value	4.0e-22
Match length	91
% identity	55
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4) >gi_902058 (U29176) lipid transfer protein precursor [Oryza

sativa]

Seq. No.	258308
Contig ID	54_3.R1011
5'-most EST	uwc700151354.h1
Method	BLASTX
NCBI GI	g4096786
BLAST score	1651
E value	0.0e+00
Match length	566
% identity	90
NCBI Description	(U39958) NADP-malic enzyme [Zea mays]

Seq. No.	258309
Contig ID	54_4.R1011
5'-most EST	LIB189-032-Q1-E1-E7
Method	BLASTX
NCBI GI	g100506
BLAST score	1232
E value	1.0e-136
Match length	251
% identity	95
NCBI Description	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria trinervia (fragment)

Seq. No.	258310
Contig ID	54_5.R1011
5'-most EST	LIB3088-004-Q1-K1-A10
Method	BLASTN
NCBI GI	g902057
BLAST score	35
E value	6.0e-10
Match length	71
% identity	87
NCBI Description	Oryza sativa lipid transfer protein precursor, mRNA, partial cds

Seq. No.	258311
Contig ID	54_6.R1011
5'-most EST	uC-zmf1b73028e11b1
Method	BLASTX
NCBI GI	g3913018
BLAST score	1515
E value	1.0e-169
Match length	349
% identity	86
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	258312
Contig ID	54_7.R1011
5'-most EST	LIB3076-027-Q1-K1-G9
Method	BLASTX
NCBI GI	g2497748
BLAST score	261
E value	3.0e-22

Match length	91
% identity	55
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4) >gi_902058 (U29176) lipid transfer protein precursor [Oryza sativa]

Seq. No.	258313
Contig ID	55_1.R1011
5'-most EST	LIB83-011-Q1-E1-B8
Method	BLASTX
NCBI GI	g1173347
BLAST score	1388
E value	1.0e-154
Match length	272
% identity	96
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No.	258314
Contig ID	56_1.R1011
5'-most EST	CPR2836_700046054_FL
Method	BLASTX
NCBI GI	g3913641
BLAST score	680
E value	1.0e-71
Match length	134
% identity	96
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	258315
Contig ID	57_5.R1011
5'-most EST	xyt700344779.h1
Method	BLASTX
NCBI GI	g4098272
BLAST score	242
E value	2.0e-24
Match length	61
% identity	100
NCBI Description	(U76558) alpha-tubulin [Triticum aestivum]

Seq. No.	258316
Contig ID	57_6.R1011
5'-most EST	LIB3060-018-Q1-K1-C5
Method	BLASTN
NCBI GI	g644492
BLAST score	160
E value	5.0e-85
Match length	233
% identity	97
NCBI Description	Corn elongation factor 1alpha gene, complete cds

Seq. No.	258317
Contig ID	57_7.R1011
5'-most EST	uC-zmflmo17118f05b1
Method	BLASTN
NCBI GI	g393400
BLAST score	149
E value	3.0e-78
Match length	197
% identity	94
NCBI Description	Z.mays mRNA for alpha-tubulin

Seq. No.	258318
Contig ID	57_8.R1011
5'-most EST	uC-zmflb73038e08a1
Method	BLASTX
NCBI GI	g2282584
BLAST score	842
E value	1.0e-90
Match length	165
% identity	97
NCBI Description	(U76259) elongation factor 1-alpha [Zea mays]

Seq. No.	258319
Contig ID	57_9.R1011
5'-most EST	xjt700092788.h1

Seq. No.	258320
Contig ID	57_10.R1011
5'-most EST	LIB3117-004-Q1-K1-A3
Method	BLASTN
NCBI GI	g485376
BLAST score	130
E value	5.0e-67
Match length	214
% identity	90
NCBI Description	Zea mays alpha-3-tubulin gene, complete cds

Seq. No.	258321
Contig ID	57_11.R1011
5'-most EST	uC-zmroteosinte048f07b1
Method	BLASTN
NCBI GI	g602605
BLAST score	119
E value	2.0e-60
Match length	251
% identity	87
NCBI Description	Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No.	258322
Contig ID	57_12.R1011
5'-most EST	wyr700236243.h1
Method	BLASTX
NCBI GI	g135417
BLAST score	253
E value	8.0e-22
Match length	63

% identity	79
NCBI Description	TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3 tubulin [Zea mays]
Seq. No.	258323
Contig ID	57_13.R1011
5'-most EST	xyt700342615.h1
Seq. No.	258324
Contig ID	57_14.R1011
5'-most EST	hvj700621936.h1
Seq. No.	258325
Contig ID	57_15.R1011
5'-most EST	LIB3067-059-Q1-K1-D1
Seq. No.	258326
Contig ID	57_16.R1011
5'-most EST	vux700157845.h1
Method	BLASTN
NCBI GI	g485376
BLAST score	74
E value	1.0e-33
Match length	142
% identity	96
NCBI Description	Zea mays alpha-3-tubulin gene, complete cds
Seq. No.	258327
Contig ID	57_17.R1011
5'-most EST	LIB3150-018-Q1-N1-B6
Method	BLASTX
NCBI GI	g232029
BLAST score	261
E value	9.0e-23
Match length	53
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_100154_pir__S21989 translation elongation factor eEF-1 alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302) elongation factor 1A [Daucus carota]
Seq. No.	258328
Contig ID	57_18.R1011
5'-most EST	tzu700207016.h1
Method	BLASTX
NCBI GI	g135417
BLAST score	431
E value	1.0e-42
Match length	97
% identity	82
NCBI Description	TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3 tubulin [Zea mays]

Seq. No.	258329
Contig ID	57_19.R1011
5'-most EST	uC-zmflmo17127e04b1

Seq. No.	258330
Contig ID	57_20.R1011
5'-most EST	LIB3150-113-P2-K1-C3
Method	BLASTX
NCBI GI	g2130149
BLAST score	152
E value	3.0e-10
Match length	30
% identity	100
NCBI Description	translation elongation factor eEF-1 alpha chain - maize (fragment)

Seq. No.	258331
Contig ID	57_21.R1011
5'-most EST	xsy700209686.h1
Method	BLASTX
NCBI GI	g1732359
BLAST score	309
E value	2.0e-28
Match length	69
% identity	88
NCBI Description	(U80268) elongation factor 1 alpha [Malus domestica]

Seq. No.	258332
Contig ID	57_22.R1011
5'-most EST	LIB3078-024-Q1-K1-H12

Seq. No.	258333
Contig ID	57_23.R1011
5'-most EST	uC-zmflmo17376e03a1
Method	BLASTN
NCBI GI	g2282583
BLAST score	59
E value	2.0e-24
Match length	115
% identity	88
NCBI Description	Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds

Seq. No.	258334
Contig ID	57_24.R1011
5'-most EST	dyk700102612.h1
Method	BLASTN
NCBI GI	g644492
BLAST score	106
E value	1.0e-52
Match length	191
% identity	88
NCBI Description	Corn elongation factor 1alpha gene, complete cds

Seq. No.	258335
Contig ID	57_25.R1011
5'-most EST	uC-zmroteosinte117g10b1

Method	BLASTX
NCBI GI	g3850818
BLAST score	174
E value	2.0e-12
Match length	31
% identity	100
NCBI Description	(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	258336
Contig ID	58_1.R1011
5'-most EST	fwa700100427.h1
Method	BLASTX
NCBI GI	g2117700
BLAST score	2350
E value	0.0e+00
Match length	517
% identity	85
NCBI Description	transketolase (EC 2.2.1.1) precursor - potato (fragment)

Seq. No.	258337
Contig ID	58_2.R1011
5'-most EST	uC-zmflmo17099c05b1
Method	BLASTX
NCBI GI	g1076746
BLAST score	2929
E value	0.0e+00
Match length	649
% identity	89
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	258338
Contig ID	58_3.R1011
5'-most EST	LIB3067-050-Q1-K1-E8
Method	BLASTX
NCBI GI	g1076746
BLAST score	2909
E value	0.0e+00
Match length	649
% identity	88
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	258339
Contig ID	58_4.R1011
5'-most EST	uC-zmroteosinte107f07b2
Method	BLASTX
NCBI GI	g4584342
BLAST score	816
E value	9.0e-88
Match length	276
% identity	62
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	258340
Contig ID	58_5.R1011
5'-most EST	nbm700472754.h1
Method	BLASTX
NCBI GI	g1076746
BLAST score	419
E value	5.0e-66
Match length	160
% identity	83
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	258341
Contig ID	58_7.R1011
5'-most EST	LIB3150-102-P2-K1-F10

Seq. No.	258342
Contig ID	58_8.R1011
5'-most EST	uC-zmflb73084f02b2
Method	BLASTX
NCBI GI	g2979565
BLAST score	470
E value	1.0e-46
Match length	124
% identity	73
NCBI Description	(AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana]

Seq. No.	258343
Contig ID	58_9.R1011
5'-most EST	LIB3150-057-Q1-N1-C6
Method	BLASTX
NCBI GI	g2979565
BLAST score	460
E value	1.0e-45
Match length	124
% identity	71
NCBI Description	(AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana]

Seq. No.	258344
Contig ID	58_10.R1011
5'-most EST	uC-zmflB73042c05b1
Method	BLASTX
NCBI GI	g2979565
BLAST score	392
E value	5.0e-38
Match length	95
% identity	76
NCBI Description	(AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana]

Seq. No.	258345
Contig ID	58_11.R1011
5'-most EST	gct701167471.h1

Seq. No.	258346
Contig ID	58_12.R1011
5'-most EST	LIB3078-050-Q1-K1-B5
Method	BLASTX
NCBI GI	g2979565
BLAST score	335
E value	5.0e-31
Match length	96
% identity	69
NCBI Description	(AC003680) putative sin3 associated polypeptide (SAP18) [Arabidopsis thaliana]

Seq. No.	258347
Contig ID	58_15.R1011
5'-most EST	uC-zmflmo17042b02b1
Method	BLASTX
NCBI GI	g1181673
BLAST score	472
E value	1.0e-59
Match length	129
% identity	87
NCBI Description	(U41652) heat shock protein cognate 70 [Sorghum bicolor]

Seq. No.	258348
Contig ID	58_18.R1011
5'-most EST	uC-zmflb73053g12b2
Method	BLASTX
NCBI GI	g629844
BLAST score	640
E value	9.0e-67
Match length	170
% identity	78
NCBI Description	heat shock protein hsp70-5 - maize (fragment) >gi_498775_emb_CAA55184_ (X78415) heat shock protein 70 kDa [Zea mays]

Seq. No.	258349
Contig ID	58_19.R1011
5'-most EST	uC-zmflmo17322f02a1

Seq. No.	258350
Contig ID	59_1.R1011
5'-most EST	CPR2864_700208152_FL
Method	BLASTX
NCBI GI	g1673456
BLAST score	900
E value	4.0e-97
Match length	170
% identity	98
NCBI Description	(Y09214) rubisco small subunit [Zea mays]

Seq. No.	258351
Contig ID	59_2.R1011
5'-most EST	LIB36-010-Q1-E1-A10
Method	BLASTX
NCBI GI	g132147

BLAST score	916
E value	6.0e-99
Match length	170
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - maize >gi_22474_emb_CAA29784_ (X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf__1312317A ribulosebisphosphate carboxylase [Zea mays]

Seq. No.	258352
Contig ID	59_3.R1011
5'-most EST	CPR2858_700100637_FL
Method	BLASTX
NCBI GI	g132147
BLAST score	917
E value	4.0e-99
Match length	170
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - maize >gi_22474_emb_CAA29784_ (X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf__1312317A ribulosebisphosphate carboxylase [Zea mays]

Seq. No.	258353
Contig ID	59_4.R1011
5'-most EST	hbs701185535.h1
Method	BLASTX
NCBI GI	g132147
BLAST score	464
E value	2.0e-69
Match length	132
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - maize >gi_22474_emb_CAA29784_ (X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf__1312317A ribulosebisphosphate carboxylase [Zea mays]

Seq. No.	258354
Contig ID	59_9.R1011
5'-most EST	LIB3078-006-Q1-K1-A3
Method	BLASTX
NCBI GI	g132147

BLAST score	188
E value	7.0e-14
Match length	45
% identity	80
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - maize >gi_22474_emb_CAA29784_ (X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf__1312317A ribulosebisphosphate carboxylase [Zea mays]

Seq. No.	258355
Contig ID	63_1.R1011
5'-most EST	LIB3069-020-Q1-K1-B3
Method	BLASTX
NCBI GI	g4262236
BLAST score	709
E value	1.0e-74
Match length	233
% identity	63
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	258356
Contig ID	63_2.R1011
5'-most EST	CPR2844_700622640_FL
Method	BLASTX
NCBI GI	g4262236
BLAST score	409
E value	1.0e-39
Match length	144
% identity	58
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	258357
Contig ID	63_3.R1011
5'-most EST	LIB143-041-Q1-E1-C3
Method	BLASTX
NCBI GI	g3420051
BLAST score	623
E value	8.0e-65
Match length	110
% identity	98
NCBI Description	(AC004680) unknown protein [Arabidopsis thaliana]

Seq. No.	258358
Contig ID	63_4.R1011
5'-most EST	uC-zmflmo17160h09b1
Method	BLASTX
NCBI GI	g3420051
BLAST score	552
E value	1.0e-59
Match length	110

% identity	98
NCBI Description	(AC004680) unknown protein [Arabidopsis thaliana]

Seq. No.	258359
Contig ID	64_1.R1011
5'-most EST	LIB3150-005-Q1-N1-A7
Method	BLASTX
NCBI GI	g1351270
BLAST score	986
E value	1.0e-107
Match length	251
% identity	75
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No.	258360
Contig ID	64_2.R1011
5'-most EST	LIB3150-118-P2-K1-C1
Method	BLASTX
NCBI GI	g1351279
BLAST score	173
E value	2.0e-12
Match length	40
% identity	85
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase [Petunia x hybrida]

Seq. No.	258361
Contig ID	65_1.R1011
5'-most EST	uC-zmflb73197d09b1
Method	BLASTX
NCBI GI	g3080369
BLAST score	327
E value	7.0e-30
Match length	196
% identity	39
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]

Seq. No.	258362
Contig ID	65_2.R1011
5'-most EST	uC-zmflb73193a08a1
Method	BLASTN
NCBI GI	g2351069
BLAST score	44
E value	2.0e-15
Match length	188
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	258363
Contig ID	65_3.R1011
5'-most EST	uC-zmflb73143c08b1
Method	BLASTX

NCBI GI	g3080369
BLAST score	258
E value	3.0e-22
Match length	105
% identity	49
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]

Seq. No.	258364
Contig ID	65_7.R1011
5'-most EST	wty700162838.h1

Seq. No.	258365
Contig ID	66_1.R1011
5'-most EST	CPR2848_700093371_FL
Method	BLASTX
NCBI GI	g1362078
BLAST score	596
E value	5.0e-74
Match length	251
% identity	59
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi_311835_emb_CAA48324_ (X68254) cellulase [Tropaeolum majus]

Seq. No.	258366
Contig ID	67_1.R1011
5'-most EST	LIB3137-033-Q1-K1-H11
Method	BLASTX
NCBI GI	g1890575
BLAST score	1255
E value	1.0e-138
Match length	274
% identity	81
NCBI Description	(X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No.	258367
Contig ID	67_2.R1011
5'-most EST	xjt700095989.h1
Method	BLASTX
NCBI GI	g1890577
BLAST score	853
E value	1.0e-91
Match length	193
% identity	79
NCBI Description	(X93175) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]

Seq. No.	258368
Contig ID	67_3.R1011
5'-most EST	uC-zmflmo17297g03b1
Method	BLASTX
NCBI GI	g1890575
BLAST score	606
E value	6.0e-63
Match length	140
% identity	76

NCBI Description	(X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]
Seq. No.	258369
Contig ID	67_4.R1011
5'-most EST	xsy700217090.h1
Seq. No.	258370
Contig ID	67_6.R1011
5'-most EST	LIB3062-004-Q1-K1-G9
Seq. No.	258371
Contig ID	67_7.R1011
5'-most EST	LIB3079-052-Q1-K1-A4
Method	BLASTX
NCBI GI	g1890575
BLAST score	541
E value	3.0e-55
Match length	141
% identity	71
NCBI Description	(X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]
Seq. No.	258372
Contig ID	67_8.R1011
5'-most EST	uC-zmf1B73007e01b1
Method	BLASTX
NCBI GI	g1890577
BLAST score	510
E value	5.0e-73
Match length	185
% identity	75
NCBI Description	(X93175) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]
Seq. No.	258373
Contig ID	67_9.R1011
5'-most EST	LIB3150-104-P2-K1-D4
Method	BLASTX
NCBI GI	g3860323
BLAST score	359
E value	7.0e-34
Match length	77
% identity	88
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.	258374
Contig ID	67_10.R1011
5'-most EST	LIB3116-006-Q1-K1-H7
Method	BLASTX
NCBI GI	g3860323
BLAST score	320
E value	2.0e-29
Match length	77
% identity	81
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	258375
Contig ID	67_14.R1011
5'-most EST	uC-zmflb73075a11a1
Method	BLASTX
NCBI GI	g3860323
BLAST score	348
E value	1.0e-32
Match length	77
% identity	87
NCBI Description	(AJ012688) hypothetical protein [Cicer arietinum]

Seq. No.	258376
Contig ID	68_1.R1011
5'-most EST	CPR2865_700208768_FL
Method	BLASTX
NCBI GI	g125580
BLAST score	1898
E value	0.0e+00
Match length	405
% identity	89
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat

Seq. No.	258377
Contig ID	69_1.R1011
5'-most EST	LIB3137-033-Q1-K1-D5
Method	BLASTX
NCBI GI	g4105561
BLAST score	1126
E value	1.0e-123
Match length	255
% identity	88
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	258378
Contig ID	69_2.R1011
5'-most EST	uC-zmflb73177f12b1
Method	BLASTX
NCBI GI	g4105561
BLAST score	553
E value	2.0e-56
Match length	134
% identity	80
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	258379
Contig ID	69_3.R1011
5'-most EST	LIB189-001-Q1-E1-F4
Method	BLASTX
NCBI GI	g4105561
BLAST score	419
E value	4.0e-41
Match length	111
% identity	78
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	258380
Contig ID	70_1.R1011
5'-most EST	LIB3116-009-Q1-K1-B10
Method	BLASTX
NCBI GI	g120657
BLAST score	198
E value	3.0e-15
Match length	38
% identity	95
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66024_pir__DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	258381
Contig ID	70_2.R1011
5'-most EST	LIB3066-033-Q1-K1-A12
Method	BLASTX
NCBI GI	g2459445
BLAST score	583
E value	1.0e-59
Match length	229
% identity	52
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	258382
Contig ID	70_3.R1011
5'-most EST	LIB3066-051-Q1-K1-F3

Seq. No.	258383
Contig ID	70_4.R1011
5'-most EST	LIB84-023-Q1-E1-A11
Method	BLASTN
NCBI GI	g22294
BLAST score	187
E value	1.0e-100
Match length	211
% identity	96
NCBI Description	Maize Gpa1 gene for glyceraldehyde-3-phosphate dehydrogenase subunit A >gi_168478_gb_M18976_MZEG3PD Zea mays chloroplast glyceraldehyde-3-phosphate dehydrogenase gene, complete cds, clone lambda-gapA1

Seq. No.	258384
Contig ID	71_1.R1011
5'-most EST	clt700042787.f1
Method	BLASTX
NCBI GI	g120663
BLAST score	1565
E value	0.0e+00
Match length	423
% identity	78
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

	CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]
Seq. No.	258385
Contig ID	71_2.R1011
5'-most EST	LIB3060-002-Q1-K2-G6
Method	BLASTX
NCBI GI	g120663
BLAST score	1726
E value	0.0e+00
Match length	448
% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR, CHLOROPLAST >gi_66027_pir__DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]
Seq. No.	258386
Contig ID	71_3.R1011
5'-most EST	LIB3115-031-P1-K1-A2
Method	BLASTX
NCBI GI	g22240
BLAST score	736
E value	4.0e-78
Match length	180
% identity	82
NCBI Description	(X07157) GADPH (383 AA) [Zea mays]
Seq. No.	258387
Contig ID	71_5.R1011
5'-most EST	LIB3137-012-Q1-K1-A11
Method	BLASTX
NCBI GI	g82166
BLAST score	575
E value	5.0e-59
Match length	158
% identity	72
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B, chloroplast - common tobacco (fragment)
Seq. No.	258388
Contig ID	71_6.R1011
5'-most EST	mwy700441070.h1
Seq. No.	258389
Contig ID	72_1.R1011
5'-most EST	CPR2855_700097674_FL
Method	BLASTX
NCBI GI	g2407233
BLAST score	252
E value	7.0e-21

Match length	101
% identity	50
NCBI Description	(AF017750) similar to Haemophilus influenzae product encoded by Genbank Accession Number U32796 [Haemophilus ducreyi]

Seq. No.	258390
Contig ID	72_2.R1011
5'-most EST	LIB3062-047-Q1-K1-H12

Seq. No.	258391
Contig ID	74_1.R1011
5'-most EST	CPR2856_700098056_FL
Method	BLASTX
NCBI GI	g3287693
BLAST score	466
E value	2.0e-46
Match length	141
% identity	68
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	258392
Contig ID	81_1.R1011
5'-most EST	xsy700210157.h1
Method	BLASTX
NCBI GI	g136063
BLAST score	1181
E value	1.0e-130
Match length	250
% identity	93
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_68426_pir__ISZMT triose-phosphate isomerase (EC 5.3.1.1) - maize >gi_168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012) triosephosphate isomerase [Zea mays]

Seq. No.	258393
Contig ID	81_2.R1011
5'-most EST	LIB3078-020-Q1-K1-C9
Method	BLASTX
NCBI GI	g136063
BLAST score	1172
E value	1.0e-129
Match length	253
% identity	91
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_68426_pir__ISZMT triose-phosphate isomerase (EC 5.3.1.1) - maize >gi_168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012) triosephosphate isomerase [Zea mays]

Seq. No.	258394
Contig ID	82_1.R1011
5'-most EST	wen700334366.h1
Method	BLASTX

NCBI GI	g4559304
BLAST score	1426
E value	1.0e-175
Match length	343
% identity	89
NCBI Description	(AF127021) T7-like RNA polymerase [Zea mays]

Seq. No.	258395
Contig ID	83_1.R1011
5'-most EST	LIB3061-052-Q1-K1-H7
Method	BLASTX
NCBI GI	g4126695
BLAST score	184
E value	4.0e-13
Match length	116
% identity	38
NCBI Description	(AB016505) prolamin [Oryza sativa]

Seq. No.	258396
Contig ID	83_2.R1011
5'-most EST	LIB3152-009-P1-K1-H1

Seq. No.	258397
Contig ID	83_4.R1011
5'-most EST	ypc700803072.h1

Seq. No.	258398
Contig ID	84_1.R1011
5'-most EST	CPR3443_700447718_FL

Seq. No.	258399
Contig ID	85_1.R1011
5'-most EST	CPR3449_700184970_FL
Method	BLASTX
NCBI GI	g121472
BLAST score	306
E value	2.0e-27
Match length	109
% identity	56
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No.	258400
Contig ID	85_2.R1011
5'-most EST	uC-zmflmo17303d08b1
Method	BLASTX
NCBI GI	g4507857
BLAST score	302
E value	1.0e-26
Match length	420
% identity	27
NCBI Description	Herpes virus-associated ubiquitin-specific protease >gi_2501460_sp_Q93009_UBPH_HUMAN PROBABLE UBIQUITIN

CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi_1545952_emb_CAA96580_ (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]

Seq. No.	258401
Contig ID	85_3.R1011
5'-most EST	LIB3151-040-Q1-K1-G9
Method	BLASTX
NCBI GI	g168695
BLAST score	267
E value	6.0e-23
Match length	105
% identity	52
NCBI Description	(M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A zein gamma [Zea mays]

Seq. No.	258402
Contig ID	85_4.R1011
5'-most EST	LIB3151-034-Q1-K1-E9
Method	BLASTX
NCBI GI	g141617
BLAST score	478
E value	7.0e-48
Match length	119
% identity	75
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir__S12140 zein Zc1 - maize >gi_100945_pir__B29017 zein 2 - maize >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays] >gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No.	258403
Contig ID	85_5.R1011
5'-most EST	LIB3059-045-Q1-K1-F10
Method	BLASTX
NCBI GI	g121472
BLAST score	333
E value	1.0e-30
Match length	90
% identity	79
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No.	258404
Contig ID	85_6.R1011
5'-most EST	LIB3152-001-Q1-K1-A7
Method	BLASTN
NCBI GI	g168484
BLAST score	258
E value	1.0e-143

Match length	423
% identity	69
NCBI Description	Maize endosperm glutelin-2 gene, complete cds

Seq. No.	258405
Contig ID	85_7.R1011
5'-most EST	LIB3061-006-Q1-K1-A8
Method	BLASTX
NCBI GI	g2832243
BLAST score	258
E value	3.0e-22
Match length	85
% identity	69
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No.	258406
Contig ID	85_8.R1011
5'-most EST	LIB3151-041-Q1-K1-C9
Method	BLASTX
NCBI GI	g121472
BLAST score	198
E value	4.0e-15
Match length	55
% identity	71
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No.	258407
Contig ID	85_10.R1011
5'-most EST	LIB3061-031-Q1-K1-G10
Method	BLASTN
NCBI GI	g22514
BLAST score	256
E value	1.0e-142
Match length	299
% identity	97
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No.	258408
Contig ID	85_11.R1011
5'-most EST	LIB3151-038-Q1-K1-C9
Method	BLASTX
NCBI GI	g168695
BLAST score	427
E value	1.0e-41
Match length	110
% identity	75
NCBI Description	(M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A zein gamma [Zea mays]

Seq. No.	258409
Contig ID	85_13.R1011
5'-most EST	hrx700704064.h1

Method	BLASTX
NCBI GI	g2668742
BLAST score	200
E value	2.0e-15
Match length	50
% identity	80
NCBI Description	(AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No.	258410
Contig ID	85_14.R1011
5'-most EST	LIB3150-109-P2-K1-B2
Method	BLASTX
NCBI GI	g168695
BLAST score	156
E value	3.0e-10
Match length	46
% identity	70
NCBI Description	(M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A zein gamma [Zea mays]

Seq. No.	258411
Contig ID	85_15.R1011
5'-most EST	LIB3061-049-Q1-K1-B10
Method	BLASTX
NCBI GI	g121472
BLAST score	206
E value	2.0e-16
Match length	42
% identity	90
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No.	258412
Contig ID	85_16.R1011
5'-most EST	LIB3151-012-Q1-K1-D5
Method	BLASTX
NCBI GI	g168695
BLAST score	203
E value	9.0e-16
Match length	69
% identity	65
NCBI Description	(M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A zein gamma [Zea mays]

Seq. No.	258413
Contig ID	85_18.R1011
5'-most EST	LIB3151-016-Q1-K1-D4
Method	BLASTX
NCBI GI	g121472
BLAST score	163
E value	6.0e-11
Match length	74
% identity	53

NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No.	258414
Contig ID	85_20.R1011
5'-most EST	ypc700804208.h1
Method	BLASTN
NCBI GI	g168694
BLAST score	197
E value	1.0e-106
Match length	343
% identity	99
NCBI Description	Maize gamma zein mRNA, partial cds

Seq. No.	258415
Contig ID	85_21.R1011
5'-most EST	LIB3059-054-Q1-K1-C7
Method	BLASTN
NCBI GI	g22514
BLAST score	147
E value	7.0e-77
Match length	194
% identity	94
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No.	258416
Contig ID	85_25.R1011
5'-most EST	ypc700801541.h1
Method	BLASTN
NCBI GI	g168484
BLAST score	177
E value	8.0e-95
Match length	229
% identity	98
NCBI Description	Maize endosperm glutelin-2 gene, complete cds

Seq. No.	258417
Contig ID	85_26.R1011
5'-most EST	LIB3059-012-Q1-K1-B1
Method	BLASTN
NCBI GI	g168484
BLAST score	88
E value	7.0e-42
Match length	88
% identity	100
NCBI Description	Maize endosperm glutelin-2 gene, complete cds

Seq. No.	258418
Contig ID	85_34.R1011
5'-most EST	LIB3059-046-Q1-K1-G4
Method	BLASTN
NCBI GI	g22516
BLAST score	125

E value	6.0e-64
Match length	228
% identity	97
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No.	258419
Contig ID	87_1.R1011
5'-most EST	CPR3490_HS5R-139-Q1-A2-C3_FL
Method	BLASTN
NCBI GI	g598955
BLAST score	1177
E value	0.0e+00
Match length	1227
% identity	99
NCBI Description	Human mRNA for hepatoma-derived growth factor, complete cds

Seq. No.	258420
Contig ID	88_1.R1011
5'-most EST	CPR3495_HS5R-152-Q1-A1-A11_FL
Method	BLASTX
NCBI GI	g337767
BLAST score	212
E value	3.0e-16
Match length	34
% identity	100
NCBI Description	(M60258) cerebroside sulfate activator protein [Homo sapiens]

Seq. No.	258421
Contig ID	89_1.R1011
5'-most EST	uC-zmflb73091h02b2
Method	BLASTX
NCBI GI	g1706374
BLAST score	1729
E value	0.0e+00
Match length	348
% identity	96
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_313678_emb_CAA28734_ (X05068) 40.1 kD A1 protein [Zea mays]

Seq. No.	258422
Contig ID	89_2.R1011
5'-most EST	uC-zmflm017084c09b1
Method	BLASTX
NCBI GI	g4096099
BLAST score	526
E value	1.0e-55
Match length	120
% identity	98
NCBI Description	(U23161) NADPH-dependent reductase [Zea mays]

Seq. No.	258423
Contig ID	89_3.R1011
5'-most EST	uC-zmflb73222c05b1
Method	BLASTX
NCBI GI	g1706374

BLAST score	849
E value	5.0e-91
Match length	219
% identity	79
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_313678_emb_CAA28734_ (X05068) 40.1 kD A1 protein [Zea mays]

Seq. No.	258424
Contig ID	89_5.R1011
5'-most EST	uC-zmflmo17317d02a1
Method	BLASTX
NCBI GI	g1706374
BLAST score	375
E value	7.0e-36
Match length	73
% identity	100
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_313678_emb_CAA28734_ (X05068) 40.1 kD A1 protein [Zea mays]

Seq. No.	258425
Contig ID	89_6.R1011
5'-most EST	uC-zmflb73360d02a1
Method	BLASTN
NCBI GI	g22102
BLAST score	353
E value	0.0e+00
Match length	377
% identity	98
NCBI Description	Zea mays A1 gene for 40.1kd A1 protein (NADPH-dependent reductase)

Seq. No.	258426
Contig ID	90_1.R1011
5'-most EST	CPR3842_700550431_FL
Method	BLASTX
NCBI GI	g3241943
BLAST score	207
E value	7.0e-16
Match length	44
% identity	82
NCBI Description	(AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No.	258427
Contig ID	91_1.R1011
5'-most EST	uC-zmflb73073d01b3
Method	BLASTX
NCBI GI	g1946371
BLAST score	421
E value	5.0e-59
Match length	325
% identity	43
NCBI Description	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No.	258428

Contig ID 91_3.R1011
5'-most EST uC-zmf1b73212c12a1

Seq. No. 258429
Contig ID 94_1.R1011
5'-most EST CPR3845_700551981_FL

Seq. No. 258430
Contig ID 95_1.R1011
5'-most EST gct701176283.h1
Method BLASTX
NCBI GI g4206306
BLAST score 218
E value 2.0e-17
Match length 119
% identity 43
NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 258431
Contig ID 95_2.R1011
5'-most EST rvt700553143.h1
Method BLASTX
NCBI GI g70772
BLAST score 410
E value 7.0e-40
Match length 82
% identity 100
NCBI Description histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden pea

Seq. No. 258432
Contig ID 95_3.R1011
5'-most EST LIB3088-029-Q1-K1-G10
Method BLASTX
NCBI GI g122106
BLAST score 363
E value 1.0e-39
Match length 102
% identity 86
NCBI Description HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 258433
Contig ID 95_4.R1011

5'-most EST	LIB3070-002-Q1-N1-C3
Method	BLASTX
NCBI GI	g122106
BLAST score	301
E value	3.0e-27
Match length	60
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	258434
Contig ID	96_1.R1011
5'-most EST	CPR5984_700044242_FL
Method	BLASTX
NCBI GI	g399307
BLAST score	684
E value	6.0e-72
Match length	235
% identity	57
NCBI Description	PRENYL TRANSFERASE >gi_99282_pir__A40433 prephytoene pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi_336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi_1016130 (U30821) prenyl transferase [Cyanophora paradoxa]

Seq. No.	258435
Contig ID	100_1.R1011
5'-most EST	LIB3137-020-Q1-K1-B4

Seq. No.	258436
Contig ID	101_1.R1011
5'-most EST	LIB3069-020-Q1-K1-E12
Method	BLASTX
NCBI GI	g4105772
BLAST score	804
E value	7.0e-86
Match length	183
% identity	53
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	258437
Contig ID	101_2.R1011
5'-most EST	cyk700049473.f1
Method	BLASTX

NCBI GI g4105772
BLAST score 379
E value 3.0e-36
Match length 92
% identity 42
NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 258438
Contig ID 101_3.R1011
5'-most EST LIB3061-021-Q1-K1-D2
Method BLASTX
NCBI GI g4105772
BLAST score 232
E value 2.0e-21
Match length 99
% identity 54
NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 258439
Contig ID 101_4.R1011
5'-most EST LIB3062-030-Q1-K1-A5

Seq. No. 258440
Contig ID 102_1.R1011
5'-most EST CPR6257_LIB81-015-Q1-E1-D5_FL
Method BLASTX
NCBI GI g2529421
BLAST score 1079
E value 1.0e-118
Match length 446
% identity 49
NCBI Description (U73935) unknown [Shewanella sp. SCRC-2738]

Seq. No. 258441
Contig ID 105_1.R1011
5'-most EST CPR6635_700802282_FL
Method BLASTX
NCBI GI g100939
BLAST score 595
E value 5.0e-80
Match length 244
% identity 68
NCBI Description zein precursor - maize

Seq. No. 258442
Contig ID 105_2.R1011
5'-most EST uC-zmflb73304a01a1
Method BLASTX
NCBI GI g4105798
BLAST score 855
E value 1.0e-91
Match length 246
% identity 54
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 258443
Contig ID 105_3.R1011

5'-most EST	LIB3180-013-P2-M1-D8
Method	BLASTX
NCBI GI	g141606
BLAST score	634
E value	6.0e-66
Match length	240
% identity	58
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) - maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No.	258444
Contig ID	105_4.R1011
5'-most EST	LIB3059-058-Q1-K1-H12
Method	BLASTX
NCBI GI	g141606
BLAST score	493
E value	2.0e-49
Match length	183
% identity	59
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) - maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No.	258445
Contig ID	105_5.R1011
5'-most EST	LIB3061-021-Q1-K1-E7
Method	BLASTX
NCBI GI	g141606
BLAST score	699
E value	1.0e-73
Match length	240
% identity	66
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) - maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No.	258446
Contig ID	105_6.R1011
5'-most EST	LIB3117-010-Q1-K1-F7
Method	BLASTX
NCBI GI	g2832243
BLAST score	684
E value	1.0e-71
Match length	237
% identity	68
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No.	258447
Contig ID	105_7.R1011
5'-most EST	LIB3059-002-Q1-K2-F3
Method	BLASTN
NCBI GI	g4140643
BLAST score	130
E value	1.0e-66
Match length	167
% identity	26

NCBI Description	Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	258448
Contig ID	105_8.R1011
5'-most EST	LIB3061-037-Q1-K1-B6
Method	BLASTX
NCBI GI	g468516
BLAST score	451
E value	2.0e-44
Match length	223
% identity	83
NCBI Description	(X55724) zein [Zea mays]
Seq. No.	258449
Contig ID	105_9.R1011
5'-most EST	LIB3061-048-Q1-K1-E2
Method	BLASTX
NCBI GI	g141613
BLAST score	589
E value	5.0e-61
Match length	140
% identity	88
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1) >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) - maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
Seq. No.	258450
Contig ID	105_10.R1011
5'-most EST	LIB3117-015-Q1-K1-C4
Method	BLASTX
NCBI GI	g2832243
BLAST score	655
E value	2.0e-68
Match length	171
% identity	80
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	258451
Contig ID	105_12.R1011
5'-most EST	LIB3061-006-Q1-K1-H10
Method	BLASTX
NCBI GI	g72307
BLAST score	343
E value	5.0e-32
Match length	144
% identity	60
NCBI Description	22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.	258452
Contig ID	105_14.R1011
5'-most EST	LIB3061-046-Q1-K1-B8
Method	BLASTX
NCBI GI	g141612
BLAST score	238
E value	7.0e-20

Match length	84
% identity	95
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2) >gi_72306_pir__ZIZMC2 22K zein precursor (clone cZ22C2) - maize (fragment) >gi_168688 (M12141) 22 kDa zein protein [Zea mays]

Seq. No.	258453
Contig ID	105_18.R1011
5'-most EST	LIB3181-008-P1-K2-F8
Method	BLASTX
NCBI GI	g22220
BLAST score	191
E value	2.0e-14
Match length	85
% identity	52
NCBI Description	(X55723) 22 kD zein [Zea mays]

Seq. No.	258454
Contig ID	105_19.R1011
5'-most EST	LIB3151-062-Q1-K1-H6
Method	BLASTX
NCBI GI	g141606
BLAST score	291
E value	1.0e-34
Match length	133
% identity	67
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) - maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No.	258455
Contig ID	105_20.R1011
5'-most EST	LIB3152-042-P1-K1-C2
Method	BLASTN
NCBI GI	g168681
BLAST score	216
E value	1.0e-118
Match length	352
% identity	91
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No.	258456
Contig ID	105_27.R1011
5'-most EST	uC-zmflmo17290c02b1
Method	BLASTX
NCBI GI	g4105798
BLAST score	410
E value	8.0e-40
Match length	201
% identity	54
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	258457
Contig ID	105_28.R1011
5'-most EST	LIB3151-049-P1-K1-H6

Method	BLASTX
NCBI GI	g141606
BLAST score	392
E value	8.0e-38
Match length	127
% identity	65
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) - maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No.	258458
Contig ID	105_29.R1011
5'-most EST	LIB3151-062-Q1-K1-A1
Method	BLASTX
NCBI GI	g141606
BLAST score	280
E value	4.0e-36
Match length	159
% identity	58
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) - maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No.	258459
Contig ID	105_30.R1011
5'-most EST	LIB3059-015-Q1-K1-C11
Method	BLASTX
NCBI GI	g141613
BLAST score	206
E value	3.0e-16
Match length	51
% identity	82
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1) >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) - maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No.	258460
Contig ID	105_37.R1011
5'-most EST	LIB3076-042-Q1-K1-A11
Method	BLASTN
NCBI GI	g4185305
BLAST score	166
E value	1.0e-88
Match length	174
% identity	99
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	258461
Contig ID	105_41.R1011
5'-most EST	ypc700804679.h1
Method	BLASTN
NCBI GI	g168681
BLAST score	46
E value	4.0e-17

Match length	121
% identity	92
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_ Sequence 8 from Patent US
Seq. No.	258462
Contig ID	106_1.R1011
5'-most EST	LIB3136-011-Q1-K1-H10
Method	BLASTX
NCBI GI	g1353135
BLAST score	305
E value	2.0e-27
Match length	140
% identity	43
NCBI Description	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR >gi_3874887_emb_CAA88100_ (Z48045) similar to serine/threonine kinase; cDNA EST EMBL:D26974 comes from this gene; cDNA EST EMBL:D26978 comes from this gene; cDNA EST EMBL:D26977 comes from this gene; cDNA EST EMBL:D26976 comes from this gene; cDNA EST E
Seq. No.	258463
Contig ID	106_2.R1011
5'-most EST	LIB83-016-Q1-E1-H9
Method	BLASTX
NCBI GI	g1353135
BLAST score	410
E value	1.0e-39
Match length	201
% identity	42
NCBI Description	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR >gi_3874887_emb_CAA88100_ (Z48045) similar to serine/threonine kinase; cDNA EST EMBL:D26974 comes from this gene; cDNA EST EMBL:D26978 comes from this gene; cDNA EST EMBL:D26977 comes from this gene; cDNA EST EMBL:D26976 comes from this gene; cDNA EST E
Seq. No.	258464
Contig ID	107_1.R1011
5'-most EST	CPR6864_700049878_FL
Method	BLASTX
NCBI GI	g2735764
BLAST score	515
E value	7.0e-52
Match length	203
% identity	52
NCBI Description	(AF008651) MADS transcriptional factor; STMADS16 [Solanum tuberosum]
Seq. No.	258465
Contig ID	109_1.R1011
5'-most EST	CPR6876_700332162_FL
Method	BLASTX
NCBI GI	g2735764
BLAST score	465
E value	5.0e-46
Match length	200

% identity	49
NCBI Description	(AF008651) MADS transcriptional factor; STMADS16 [Solanum tuberosum]

Seq. No.	258466
Contig ID	109_2.R1011
5'-most EST	LIB189-012-Q1-E1-F6
Method	BLASTX
NCBI GI	g2735764
BLAST score	424
E value	3.0e-41
Match length	190
% identity	47
NCBI Description	(AF008651) MADS transcriptional factor; STMADS16 [Solanum tuberosum]

Seq. No.	258467
Contig ID	111_1.R1011
5'-most EST	pmx700083990.h1
Method	BLASTX
NCBI GI	g4322475
BLAST score	287
E value	3.0e-25
Match length	90
% identity	64
NCBI Description	(AF086642) putative MADS box transcription factor ETL [Eucalyptus globulus subsp. globulus]

Seq. No.	258468
Contig ID	112_1.R1011
5'-most EST	uC-zmflb73200b03b1
Method	BLASTX
NCBI GI	g2979566
BLAST score	458
E value	3.0e-45
Match length	210
% identity	50
NCBI Description	(AC003680) MADS box protein AGL20 [Arabidopsis thaliana]

Seq. No.	258469
Contig ID	112_3.R1011
5'-most EST	yyf700348009.h1
Method	BLASTX
NCBI GI	g695690
BLAST score	284
E value	2.0e-25
Match length	61
% identity	92
NCBI Description	(X79281) DAL3 protein [Picea abies]

Seq. No.	258470
Contig ID	113_1.R1011
5'-most EST	CPR6875_700282564_FL
Method	BLASTX
NCBI GI	g1905930
BLAST score	1013
E value	1.0e-110

Match length	240
% identity	83
NCBI Description	(U31994) MADS box protein [Oryza sativa]

Seq. No.	258471
Contig ID	113_2.R1011
5'-most EST	uC-zmflmo17263a07b1
Method	BLASTX
NCBI GI	g3851333
BLAST score	1180
E value	1.0e-130
Match length	231
% identity	97
NCBI Description	(Y09302) putative MADS-domain transcription factor [Zea mays]

Seq. No.	258472
Contig ID	113_3.R1011
5'-most EST	CPR6888_700468216_FL
Method	BLASTX
NCBI GI	g1483232
BLAST score	594
E value	4.0e-61
Match length	248
% identity	54
NCBI Description	(X99655) MADS5 protein [Betula pendula]

Seq. No.	258473
Contig ID	113_4.R1011
5'-most EST	CPR6882_700350443_FL
Method	BLASTX
NCBI GI	g3851333
BLAST score	1155
E value	1.0e-127
Match length	230
% identity	97
NCBI Description	(Y09302) putative MADS-domain transcription factor [Zea mays]

Seq. No.	258474
Contig ID	113_5.R1011
5'-most EST	uC-zmflB73045d06b1
Method	BLASTX
NCBI GI	g4204232
BLAST score	768
E value	2.0e-81
Match length	245
% identity	65
NCBI Description	(AF035378) MADS-box protein 1 [Lolium temulentum]

Seq. No.	258475
Contig ID	113_6.R1011
5'-most EST	LIB3068-061-Q1-K1-D4
Method	BLASTX
NCBI GI	g3851333
BLAST score	1155
E value	1.0e-127

Match length	230
% identity	97
NCBI Description	(Y09302) putative MADS-domain transcription factor [Zea mays]

Seq. No.	258476
Contig ID	113_7.R1011
5'-most EST	uC-zmflmo17035a10b1
Method	BLASTX
NCBI GI	g4204232
BLAST score	762
E value	8.0e-81
Match length	244
% identity	65
NCBI Description	(AF035378) MADS-box protein 1 [Lolium temulentum]

Seq. No.	258477
Contig ID	113_8.R1011
5'-most EST	uC-zmflmo17030g11b1
Method	BLASTX
NCBI GI	g2286111
BLAST score	280
E value	1.0e-24
Match length	89
% identity	64
NCBI Description	(U78891) MADS box protein [Oryza sativa]

Seq. No.	258478
Contig ID	116_1.R1011
5'-most EST	CPR6892_700612251_FL
Method	BLASTX
NCBI GI	g886401
BLAST score	999
E value	1.0e-108
Match length	209
% identity	91
NCBI Description	(L37526) MADS box protein [Oryza sativa]

Seq. No.	258479
Contig ID	119_1.R1011
5'-most EST	uC-zmflb73020h04b1
Method	BLASTX
NCBI GI	g939785
BLAST score	281
E value	9.0e-30
Match length	132
% identity	61
NCBI Description	(L46400) MADS box protein [Zea mays]

Seq. No.	258480
Contig ID	120_1.R1011
5'-most EST	LIB3088-005-Q1-K1-C12
Method	BLASTX
NCBI GI	g3892652
BLAST score	390
E value	3.0e-37
Match length	104

% identity	76
NCBI Description	(Y09303) putative MADS-domain transcription factor [Zea mays]

Seq. No.	258481
Contig ID	120_2.R1011
5'-most EST	LIB3067-059-Q1-K1-A11
Method	BLASTX
NCBI GI	g3892652
BLAST score	639
E value	1.0e-66
Match length	155
% identity	83
NCBI Description	(Y09303) putative MADS-domain transcription factor [Zea mays]

Seq. No.	258482
Contig ID	120_3.R1011
5'-most EST	LIB3067-032-Q1-K1-B1
Method	BLASTX
NCBI GI	g3892652
BLAST score	419
E value	2.0e-41
Match length	103
% identity	84
NCBI Description	(Y09303) putative MADS-domain transcription factor [Zea mays]

Seq. No.	258483
Contig ID	123_1.R1011
5'-most EST	fdz701160751.h1
Method	BLASTX
NCBI GI	g2961437
BLAST score	907
E value	7.0e-98
Match length	212
% identity	80
NCBI Description	(L37527) MADS box protein [Oryza sativa]

Seq. No.	258484
Contig ID	124_1.R1011
5'-most EST	CPR6886_700434680_FL
Method	BLASTX
NCBI GI	g3493647
BLAST score	217
E value	3.0e-17
Match length	126
% identity	42
NCBI Description	(AF082531) transcription activator [Pimpinella brachycarpa]

Seq. No.	258485
Contig ID	126_1.R1011
5'-most EST	uC-zmf1b73062g04b1
Method	BLASTX
NCBI GI	g3646324
BLAST score	417
E value	3.0e-58

Match length 239
% identity 58
NCBI Description (AJ000761) MADS-box protein [Malus domestica]

Seq. No. 258486
Contig ID 129_1.R1011
5'-most EST pwr700450237.h1
Method BLASTX
NCBI GI g2281705
BLAST score 2200
E value 0.0e+00
Match length 539
% identity 81
NCBI Description (AF013979) ethylene responsive factor [Oryza sativa]

Seq. No. 258487
Contig ID 129_2.R1011
5'-most EST uC-zmflmo17059f05a1

Seq. No. 258488
Contig ID 130_1.R1011
5'-most EST xsy700212586.h1
Method BLASTX
NCBI GI g4105633
BLAST score 1127
E value 1.0e-123
Match length 549
% identity 46
NCBI Description (AF048982) putative ethylene receptor [Arabidopsis thaliana]

Seq. No. 258489
Contig ID 130_2.R1011
5'-most EST tzu700203005.h1
Method BLASTX
NCBI GI g4105633
BLAST score 195
E value 3.0e-15
Match length 97
% identity 45
NCBI Description (AF048982) putative ethylene receptor [Arabidopsis thaliana]

Seq. No. 258490
Contig ID 132_1.R1011
5'-most EST LIB3076-044-Q1-K1-E5
Method BLASTX
NCBI GI g3913427
BLAST score 2087
E value 0.0e+00
Match length 400
% identity 100
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 258491

Contig ID	132_2.R1011
5'-most EST	LIB189-030-Q1-E1-D11
Method	BLASTX
NCBI GI	g3913427
BLAST score	1111
E value	1.0e-122
Match length	242
% identity	87
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No.	258492
Contig ID	132_3.R1011
5'-most EST	LIB3137-035-Q1-K1-B5
Method	BLASTX
NCBI GI	g2129921
BLAST score	163
E value	9.0e-11
Match length	36
% identity	83
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	258493
Contig ID	132_4.R1011
5'-most EST	qmh700029323.f1
Method	BLASTN
NCBI GI	g1532072
BLAST score	289
E value	1.0e-161
Match length	301
% identity	99
NCBI Description	Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No.	258494
Contig ID	132_6.R1011
5'-most EST	uC-zmflmo17336b03b1
Method	BLASTX
NCBI GI	g2129921
BLAST score	165
E value	3.0e-11
Match length	43
% identity	70
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	258495
Contig ID	132_8.R1011
5'-most EST	uC-zmflmo17125d12b1
Method	BLASTX
NCBI GI	g2131329
BLAST score	157
E value	5.0e-10
Match length	56
% identity	50
NCBI Description	hypothetical protein YDL087c - yeast (Saccharomyces

cerevisiae) >gi_1431114_emb_CAA98653_ (Z74135) ORF YDL087c [Saccharomyces cerevisiae]

Seq. No.	258496
Contig ID	132_9.R1011
5'-most EST	tfd700572020.h1
Method	BLASTX
NCBI GI	g3913427
BLAST score	706
E value	4.0e-74
Match length	144
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No.	258497
Contig ID	132_10.R1011
5'-most EST	uC-zmflMo17002c08b1
Method	BLASTX
NCBI GI	g2131329
BLAST score	152
E value	1.0e-09
Match length	48
% identity	58
NCBI Description	hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae) >gi_1431114_emb_CAA98653_ (Z74135) ORF YDL087c [Saccharomyces cerevisiae]

Seq. No.	258498
Contig ID	132_11.R1011
5'-most EST	yyf700351472.h1
Method	BLASTX
NCBI GI	g2213558
BLAST score	157
E value	1.0e-09
Match length	88
% identity	45
NCBI Description	(Z97052) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	258499
Contig ID	132_12.R1011
5'-most EST	LIB3067-035-Q1-K1-H9
Method	BLASTX
NCBI GI	g3913427
BLAST score	625
E value	2.0e-65
Match length	125
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No.	258500
Contig ID	132_14.R1011
5'-most EST	uC-zmflMo17010b07b1
Method	BLASTX

NCBI GI	g2129921
BLAST score	152
E value	1.0e-09
Match length	34
% identity	79
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	258501
Contig ID	132_16.R1011
5'-most EST	uC-zmflmo17288d05b1

Seq. No.	258502
Contig ID	132_17.R1011
5'-most EST	uC-zmrob73076g12b1
Method	BLASTX
NCBI GI	g2129921
BLAST score	167
E value	2.0e-11
Match length	36
% identity	83
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

Seq. No.	258503
Contig ID	132_20.R1011
5'-most EST	LIB3069-042-Q1-K1-A11
Method	BLASTN
NCBI GI	g1532072
BLAST score	191
E value	1.0e-103
Match length	234
% identity	96
NCBI Description	Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No.	258504
Contig ID	132_22.R1011
5'-most EST	uC-zmflmo17061d09b1
Method	BLASTX
NCBI GI	g3913427
BLAST score	648
E value	1.0e-78
Match length	182
% identity	88
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No.	258505
Contig ID	132_26.R1011
5'-most EST	LIB3137-028-Q1-K1-A3
Method	BLASTN
NCBI GI	g1532072
BLAST score	115
E value	6.0e-58
Match length	139
% identity	96

NCBI Description	Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.	258506
Contig ID	132_28.R1011
5'-most EST	uC-zmflmo17221d07a1
Seq. No.	258507
Contig ID	132_29.R1011
5'-most EST	uC-zmflMo17004c08b1
Seq. No.	258508
Contig ID	132_30.R1011
5'-most EST	uC-zmflb73064a03b1
Method	BLASTX
NCBI GI	g3913427
BLAST score	564
E value	9.0e-58
Match length	116
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.	258509
Contig ID	132_32.R1011
5'-most EST	LIB3069-036-Q1-K1-A4
Seq. No.	258510
Contig ID	132_40.R1011
5'-most EST	LIB3150-055-Q1-N1-C2
Method	BLASTN
NCBI GI	g1532072
BLAST score	34
E value	1.0e-09
Match length	38
% identity	97
NCBI Description	Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.	258511
Contig ID	132_42.R1011
5'-most EST	gwl700616273.h1
Method	BLASTN
NCBI GI	g1532072
BLAST score	127
E value	4.0e-65
Match length	135
% identity	99
NCBI Description	Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.	258512
Contig ID	134_1.R1011
5'-most EST	uC-zmflb73028g02b1
Method	BLASTX
NCBI GI	g2580499
BLAST score	2113
E value	0.0e+00
Match length	565

% identity	71
NCBI Description	(U67186) NADPH:ferrihemoprotein oxidoreductase [Eschscholzia californica]

Seq. No.	258513
Contig ID	134_2.R1011
5'-most EST	uC-zmflmo17341a07b1

Seq. No.	258514
Contig ID	134_3.R1011
5'-most EST	LIB3078-040-Q1-K1-E8
Method	BLASTX
NCBI GI	g2809385
BLAST score	677
E value	5.0e-71
Match length	155
% identity	79
NCBI Description	(AF024634) NADPH cytochrome P450 reductase [Petroselinum crispum]

Seq. No.	258515
Contig ID	134_5.R1011
5'-most EST	xsy700208936.h1
Method	BLASTX
NCBI GI	g2809385
BLAST score	603
E value	2.0e-62
Match length	144
% identity	76
NCBI Description	(AF024634) NADPH cytochrome P450 reductase [Petroselinum crispum]

Seq. No.	258516
Contig ID	134_9.R1011
5'-most EST	LIB3067-037-Q1-K1-H12

Seq. No.	258517
Contig ID	134_14.R1011
5'-most EST	ypc700798870.h1
Method	BLASTX
NCBI GI	g1006694
BLAST score	246
E value	2.0e-21
Match length	62
% identity	69
NCBI Description	(Z49767) NADPH-cytochrome P450 reductase [Pseudotsuga menziesii]

Seq. No.	258518
Contig ID	135_6.R1011
5'-most EST	uwc700154463.h1

Seq. No.	258519
Contig ID	135_7.R1011
5'-most EST	cyk700049132.f1
Method	BLASTX
NCBI GI	g1173055

BLAST score	244
E value	3.0e-34
Match length	82
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No.	258520
Contig ID	135_8.R1011
5'-most EST	LIB143-052-Q1-E1-A1
Method	BLASTX
NCBI GI	g1173055
BLAST score	342
E value	2.0e-32
Match length	66
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No.	258521
Contig ID	135_9.R1011
5'-most EST	uC-zmroteosinte047f12b2

Seq. No.	258522
Contig ID	135_10.R1011
5'-most EST	LIB3067-033-Q1-K1-G6

Seq. No.	258523
Contig ID	135_11.R1011
5'-most EST	wty700167572.h1
Method	BLASTX
NCBI GI	g3377851
BLAST score	163
E value	4.0e-11
Match length	49
% identity	65
NCBI Description	(AF076274) contains similarity to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 155.05) [Arabidopsis thaliana]

Seq. No.	258524
Contig ID	135_12.R1011
5'-most EST	wty700171561.h1
Method	BLASTX
NCBI GI	g462013
BLAST score	221
E value	3.0e-18
Match length	47
% identity	96
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	258525
Contig ID	135_13.R1011
5'-most EST	nbm700466246.h1
Method	BLASTX
NCBI GI	g3123270
BLAST score	283
E value	2.0e-33
Match length	82
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620) >gi_2463335_emb_CAA75242_ (Y15009) ribosomal protein S4 [Oryza sativa]

Seq. No.	258526
Contig ID	135_14.R1011
5'-most EST	gct701178281.h1
Method	BLASTX
NCBI GI	g4006914
BLAST score	302
E value	2.0e-27
Match length	66
% identity	80
NCBI Description	(Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]

Seq. No.	258527
Contig ID	135_15.R1011
5'-most EST	LIB3067-023-Q1-K1-D4
Method	BLASTX
NCBI GI	g4455246
BLAST score	195
E value	7.0e-15
Match length	59
% identity	59
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	258528
Contig ID	135_16.R1011
5'-most EST	uC-zmflmo17035c10b1

Seq. No.	258529
Contig ID	135_17.R1011
5'-most EST	hvj700623950.h1

Seq. No.	258530
Contig ID	135_18.R1011
5'-most EST	LIB143-030-Q1-E1-H5

Seq. No.	258531
Contig ID	135_19.R1011
5'-most EST	uC-zmflmo17128h07b1
Method	BLASTX
NCBI GI	g2980794
BLAST score	391
E value	6.0e-38
Match length	90

% identity	74
NCBI Description	(AL022197) myb - like protein [Arabidopsis thaliana]

Seq. No.	258532
Contig ID	135_20.R1011
5'-most EST	LIB3060-035-Q1-K1-F9
Method	BLASTX
NCBI GI	g1172817
BLAST score	293
E value	2.0e-26
Match length	74
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_ (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]

Seq. No.	258533
Contig ID	135_21.R1011
5'-most EST	uC-zmflmo17293c11b1

Seq. No.	258534
Contig ID	135_22.R1011
5'-most EST	mwy700439712.h1
Method	BLASTN
NCBI GI	g22614
BLAST score	39
E value	2.0e-12
Match length	63
% identity	90
NCBI Description	S.vulgare pepC gene for PEP carboxylase

Seq. No.	258535
Contig ID	135_23.R1011
5'-most EST	LIB3088-002-Q1-K1-B2

Seq. No.	258536
Contig ID	135_24.R1011
5'-most EST	fwa700100017.h1
Method	BLASTX
NCBI GI	g729442
BLAST score	194
E value	8.0e-15
Match length	75
% identity	52
NCBI Description	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi_166380 (M80235) glucose-regulated endoplasmic reticular protein precursor [Medicago sativa]

Seq. No.	258537
Contig ID	135_25.R1011
5'-most EST	uC-zmflb73359e06a2
Method	BLASTX
NCBI GI	g3687389
BLAST score	207
E value	2.0e-16
Match length	67

% identity	66
NCBI Description	(Y16124) putative cullin protein [Lycopersicon esculentum]
Seq. No.	258538
Contig ID	135_26.R1011
5'-most EST	LIB3062-027-Q1-K1-F7
Seq. No.	258539
Contig ID	135_27.R1011
5'-most EST	ymt700221253.h1
Seq. No.	258540
Contig ID	135_28.R1011
5'-most EST	ntr700077051.h1
Method	BLASTX
NCBI GI	g4249419
BLAST score	198
E value	5.0e-15
Match length	82
% identity	50
NCBI Description	(AC006072) hypothetical protein, 3' partial [Arabidopsis thaliana]
Seq. No.	258541
Contig ID	135_29.R1011
5'-most EST	pmx700083985.h1
Seq. No.	258542
Contig ID	135_30.R1011
5'-most EST	LIB3279-057-P1-K1-F4
Method	BLASTX
NCBI GI	g4006914
BLAST score	409
E value	8.0e-40
Match length	150
% identity	55
NCBI Description	(Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]
Seq. No.	258543
Contig ID	135_31.R1011
5'-most EST	uC-zmflb73204h08b1
Seq. No.	258544
Contig ID	135_32.R1011
5'-most EST	wty700163472.h1
Method	BLASTN
NCBI GI	g529093
BLAST score	67
E value	5.0e-29
Match length	184
% identity	84
NCBI Description	Rice mRNA for proteasome C2 subunit, complete cds
Seq. No.	258545
Contig ID	135_33.R1011
5'-most EST	LIB3151-048-P1-K1-D3

Method	BLASTX
NCBI GI	g4455349
BLAST score	195
E value	9.0e-15
Match length	151
% identity	34
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	258546
Contig ID	135_34.R1011
5'-most EST	uC-zmflb73100f09b1
Method	BLASTX
NCBI GI	g3377851
BLAST score	175
E value	2.0e-12
Match length	44
% identity	75
NCBI Description	(AF076274) contains similarity to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 155.05) [Arabidopsis thaliana]

Seq. No.	258547
Contig ID	135_35.R1011
5'-most EST	mwy700439817.h1
Method	BLASTX
NCBI GI	g1709758
BLAST score	306
E value	4.0e-47
Match length	107
% identity	93
NCBI Description	PROTEASOME COMPONENT C2 (MACROPAIN SUBUNIT C2) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2) >gi_1066151_dbj_BAA07128_ (D37886) proteasome C2 subunit [Oryza sativa]

Seq. No.	258548
Contig ID	135_36.R1011
5'-most EST	xdb700341364.h1

Seq. No.	258549
Contig ID	135_37.R1011
5'-most EST	vux700160160.h1
Method	BLASTN
NCBI GI	g2832242
BLAST score	80
E value	7.0e-37
Match length	141
% identity	96
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	258550
Contig ID	135_38.R1011
5'-most EST	uC-zmflb73067g08a1
Method	BLASTX
NCBI GI	g2689720
BLAST score	288
E value	6.0e-26

Match length	113
% identity	52
NCBI Description	(AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No.	258551
Contig ID	135_39.R1011
5'-most EST	uC-zmflmo17397d07a1
Method	BLASTX
NCBI GI	g544242
BLAST score	236
E value	7.0e-20
Match length	57
% identity	84
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]

Seq. No.	258552
Contig ID	135_40.R1011
5'-most EST	rvl700455748.h1
Method	BLASTX
NCBI GI	g3377851
BLAST score	161
E value	1.0e-10
Match length	38
% identity	79
NCBI Description	(AF076274) contains similarity to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 155.05) [Arabidopsis thaliana]

Seq. No.	258553
Contig ID	135_41.R1011
5'-most EST	LIB3075-043-Q1-K1-A6
Method	BLASTX
NCBI GI	g3914899
BLAST score	331
E value	2.0e-30
Match length	90
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]

Seq. No.	258554
Contig ID	135_42.R1011
5'-most EST	uC-zmflb73051f02b1

Seq. No.	258555
Contig ID	135_43.R1011
5'-most EST	xmt700266058.h1

Seq. No.	258556
Contig ID	135_44.R1011
5'-most EST	fdz701164992.h1
Method	BLASTX
NCBI GI	g3549652
BLAST score	212

E value 2.0e-16
Match length 67
% identity 64
NCBI Description (AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No. 258557
Contig ID 135_45.R1011
5'-most EST uC-zmflmo17283b03b1
Method BLASTX
NCBI GI g3914899
BLAST score 428
E value 6.0e-42
Match length 94
% identity 88
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]

Seq. No. 258558
Contig ID 135_46.R1011
5'-most EST LIB143-026-Q1-E1-F3
Method BLASTX
NCBI GI g3549652
BLAST score 581
E value 9.0e-60
Match length 298
% identity 48
NCBI Description (AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No. 258559
Contig ID 135_47.R1011
5'-most EST mwy700441514.h1
Method BLASTX
NCBI GI g1488521
BLAST score 321
E value 3.0e-29
Match length 241
% identity 54
NCBI Description (X99938) RNA helicase [Arabidopsis thaliana]

Seq. No. 258560
Contig ID 135_48.R1011
5'-most EST uC-zmflb73346e10a2
Method BLASTX
NCBI GI g544242
BLAST score 507
E value 2.0e-51
Match length 128
% identity 81
NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]

Seq. No. 258561
Contig ID 135_49.R1011

5'-most EST	LIB3115-015-P1-K1-H6
Method	BLASTX
NCBI GI	g4204293
BLAST score	158
E value	2.0e-10
Match length	118
% identity	32
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	258562
Contig ID	135_50.R1011
5'-most EST	LIB189-004-Q1-E1-G5
Method	BLASTX
NCBI GI	g462013
BLAST score	165
E value	4.0e-11
Match length	34
% identity	100
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	258563
Contig ID	135_51.R1011
5'-most EST	LIB3069-005-Q1-K1-F10
Method	BLASTX
NCBI GI	g3549652
BLAST score	384
E value	6.0e-37
Match length	92
% identity	83
NCBI Description	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]

Seq. No.	258564
Contig ID	135_52.R1011
5'-most EST	nbm700472333.h1
Method	BLASTX
NCBI GI	g544242
BLAST score	423
E value	2.0e-41
Match length	93
% identity	90
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]

Seq. No.	258565
Contig ID	135_53.R1011
5'-most EST	xsy700217062.h1
Method	BLASTX
NCBI GI	g3377805
BLAST score	699
E value	2.0e-73

Match length	254
% identity	53
NCBI Description	(AF075597) contains similarity to several apoptosis or programmed cell death proteins such as rat apoptosis protein RP-8 (GB:M80601) [Arabidopsis thaliana] >gi_3912928_gb_AAC78712.1_ (AF001308) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	258566
Contig ID	135_54.R1011
5'-most EST	ntr700074435.h1
Method	BLASTX
NCBI GI	g4006914
BLAST score	161
E value	9.0e-11
Match length	81
% identity	47
NCBI Description	(Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]

Seq. No.	258567
Contig ID	135_55.R1011
5'-most EST	ypc700803409.h1
Method	BLASTX
NCBI GI	g1167955
BLAST score	201
E value	2.0e-15
Match length	116
% identity	38
NCBI Description	(U43497) putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein [Hordeum vulgare]

Seq. No.	258568
Contig ID	135_56.R1011
5'-most EST	LIB3136-056-Q1-K1-G1
Method	BLASTN
NCBI GI	g2345153
BLAST score	53
E value	1.0e-20
Match length	115
% identity	96
NCBI Description	Zea mays ribsomal protein S4 (rps4) mRNA, complete cds

Seq. No.	258569
Contig ID	135_57.R1011
5'-most EST	wty700168530.h1
Method	BLASTX
NCBI GI	g1488647
BLAST score	187
E value	1.0e-13
Match length	103
% identity	38
NCBI Description	(X99937) RNA helicase [Spinacia oleracea]

Seq. No.	258570
Contig ID	135_58.R1011

5'-most EST	uC-zmrob73049d01a1
Method	BLASTX
NCBI GI	g4455246
BLAST score	201
E value	4.0e-15
Match length	59
% identity	63
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	258571
Contig ID	135_59.R1011
5'-most EST	LIB143-063-Q1-E1-A11
Method	BLASTX
NCBI GI	g3377805
BLAST score	581
E value	3.0e-73
Match length	255
% identity	55
NCBI Description	(AF075597) contains similarity to several apoptosis or programmed cell death proteins such as rat apoptosis protein RP-8 (GB:M80601) [Arabidopsis thaliana] >gi_3912928_gb_AAC78712.1_ (AF001308) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	258572
Contig ID	135_60.R1011
5'-most EST	ntr700072029.h1
Method	BLASTN
NCBI GI	g2832242
BLAST score	99
E value	6.0e-48
Match length	213
% identity	92
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	258573
Contig ID	141_1.R1011
5'-most EST	CPR9116consensus_FL
Method	BLASTX
NCBI GI	g3618320
BLAST score	171
E value	1.0e-11
Match length	100
% identity	40
NCBI Description	(AB001888) zinc finger protein [Oryza sativa]

Seq. No.	258574
Contig ID	142_1.R1011
5'-most EST	xmt700264303.h1
Method	BLASTX
NCBI GI	g4539315
BLAST score	514
E value	9.0e-52
Match length	202
% identity	51
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	258575
Contig ID	142_2.R1011
5'-most EST	CPR9117consensus_FL
Method	BLASTX
NCBI GI	g4539315
BLAST score	518
E value	4.0e-52
Match length	206
% identity	51
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	258576
Contig ID	142_5.R1011
5'-most EST	dyk700104747.h1
Method	BLASTX
NCBI GI	g2052090
BLAST score	363
E value	1.0e-34
Match length	89
% identity	80
NCBI Description	(Z49145) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No.	258577
Contig ID	143_1.R1011
5'-most EST	CPR9150_700620948_FL
Method	BLASTN
NCBI GI	g500852
BLAST score	53
E value	6.0e-21
Match length	73
% identity	93
NCBI Description	Zea mays (clone pAKHSDH2) aspartate kinase-homoserine dehydrogenase mRNA, complete cds

Seq. No.	258578
Contig ID	144_1.R1011
5'-most EST	CPR9153_7001180088_FL
Method	BLASTX
NCBI GI	g1362086
BLAST score	324
E value	5.0e-30
Match length	68
% identity	93
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	258579
Contig ID	145_1.R1011
5'-most EST	CPR917_700209591_FL
Method	BLASTX

NCBI GI	g1850968
BLAST score	596
E value	2.0e-61
Match length	222
% identity	53
NCBI Description	(U79733) Hs1pro-1 [Beta procumbens]

Seq. No.	258580
Contig ID	145_2.R1011
5'-most EST	CPR919_700104751_FL

Seq. No.	258581
Contig ID	148_1.R1011
5'-most EST	uC-zmf1b73283e03b2
Method	BLASTX
NCBI GI	g4376158
BLAST score	194
E value	2.0e-24
Match length	124
% identity	56
NCBI Description	(X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No.	258582
Contig ID	149_1.R1011
5'-most EST	CPR9204_700096779_FL
Method	BLASTX
NCBI GI	g1351904
BLAST score	2626
E value	0.0e+00
Match length	920
% identity	99
NCBI Description	ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST PRECURSOR (AK-HSDH 1) (AKHSDH1) >gi_500851 (L33912) aspartate kinase-homoserine dehydrogenase [Zea mays]

Seq. No.	258583
Contig ID	150_1.R1011
5'-most EST	CPR9205_700086788_FL
Method	BLASTX
NCBI GI	g2198851
BLAST score	2138
E value	0.0e+00
Match length	483
% identity	98
NCBI Description	(AF007785) cystathionine gamma-synthase [Zea mays]

Seq. No.	258584
Contig ID	150_3.R1011
5'-most EST	uC-zmrob73061b04a1
Method	BLASTX
NCBI GI	g2198851
BLAST score	208
E value	3.0e-16
Match length	50
% identity	90
NCBI Description	(AF007785) cystathionine gamma-synthase [Zea mays]

Seq. No.	258585
Contig ID	151_1.R1011
5'-most EST	LIB3279-005-P1-K1-C2
Method	BLASTX
NCBI GI	g1170937
BLAST score	1952
E value	0.0e+00
Match length	396
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258586
Contig ID	151_2.R1011
5'-most EST	uC-zmflmo17057d08b1
Method	BLASTN
NCBI GI	g22091
BLAST score	316
E value	1.0e-177
Match length	608
% identity	38
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258587
Contig ID	151_3.R1011
5'-most EST	uC-zmflmo17070b11b1
Method	BLASTX
NCBI GI	g1170937
BLAST score	1955
E value	0.0e+00
Match length	396
% identity	95
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258588
Contig ID	151_4.R1011
5'-most EST	uC-zmflmo17267g02a1
Method	BLASTN
NCBI GI	g22091
BLAST score	299
E value	1.0e-167
Match length	415
% identity	95
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258589
Contig ID	151_5.R1011
5'-most EST	uC-zmflb73152h01b1
Method	BLASTX
NCBI GI	g1076316
BLAST score	279
E value	3.0e-24

Match length	218
% identity	33
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	258590
Contig ID	151_6.R1011
5'-most EST	LIB3060-035-Q1-K1-H3
Method	BLASTX
NCBI GI	g1170937
BLAST score	1945
E value	0.0e+00
Match length	396
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258591
Contig ID	151_7.R1011
5'-most EST	uC-zmflmo17030b05b1
Method	BLASTN
NCBI GI	g22332
BLAST score	436
E value	0.0e+00
Match length	729
% identity	50
NCBI Description	Z.mays HRGP gene

Seq. No.	258592
Contig ID	151_8.R1011
5'-most EST	uC-zmflmo17335f11b1
Method	BLASTN
NCBI GI	g257040
BLAST score	499
E value	0.0e+00
Match length	1051
% identity	55
NCBI Description	hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No.	258593
Contig ID	151_9.R1011
5'-most EST	bdu700382902.h1
Method	BLASTX
NCBI GI	g1495251
BLAST score	1751
E value	0.0e+00
Match length	529
% identity	66
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258594
Contig ID	151_10.R1011
5'-most EST	uC-zmflb73001e08b1
Method	BLASTX

NCBI GI	g1495251
BLAST score	1412
E value	1.0e-157
Match length	491
% identity	59
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258595
Contig ID	151_11.R1011
5'-most EST	tzu700203924.h1
Method	BLASTX
NCBI GI	g1495251
BLAST score	2005
E value	0.0e+00
Match length	612
% identity	68
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258596
Contig ID	151_12.R1011
5'-most EST	uC-zmflb73414h02a1

Seq. No.	258597
Contig ID	151_13.R1011
5'-most EST	uC-zmflmo17335a04b1
Method	BLASTX
NCBI GI	g2129677
BLAST score	208
E value	3.0e-16
Match length	79
% identity	54
NCBI Description	probable1 N-acetyltransferase hookless 1 - Arabidopsis thaliana >gi_1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_4468983_emb_CAB38297_ (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

Seq. No.	258598
Contig ID	151_14.R1011
5'-most EST	uC-zmflmo17046g11b1
Method	BLASTN
NCBI GI	g22332
BLAST score	312
E value	1.0e-175
Match length	383
% identity	95
NCBI Description	Z.mays HRGP gene

Seq. No.	258599
Contig ID	151_15.R1011
5'-most EST	LIB3078-032-Q1-K1-D1
Method	BLASTX
NCBI GI	g1170937
BLAST score	651
E value	5.0e-68
Match length	149

% identity	87
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258600
Contig ID	151_16.R1011
5'-most EST	uC-zmflB73004h10b1
Method	BLASTN
NCBI GI	g22507
BLAST score	457
E value	0.0e+00
Match length	502
% identity	98
NCBI Description	Maize (strain W64A) mRNA for cell wall glycoprotein

Seq. No.	258601
Contig ID	151_17.R1011
5'-most EST	gwl700616344.h1
Method	BLASTX
NCBI GI	g3941289
BLAST score	814
E value	6.0e-87
Match length	266
% identity	56
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No.	258602
Contig ID	151_18.R1011
5'-most EST	wty700167803.h1
Method	BLASTX
NCBI GI	g1076316
BLAST score	250
E value	8.0e-21
Match length	188
% identity	34
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	258603
Contig ID	151_19.R1011
5'-most EST	uC-zmroteosinte069f12b1
Method	BLASTX
NCBI GI	g1170937
BLAST score	596
E value	1.0e-61
Match length	124
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258604
Contig ID	151_20.R1011

5'-most EST	LIB3069-006-Q1-K1-D5
Method	BLASTX
NCBI GI	g1170937
BLAST score	364
E value	1.0e-34
Match length	74
% identity	95
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258605
Contig ID	151_21.R1011
5'-most EST	uC-zmflmo17151b05b1
Method	BLASTN
NCBI GI	g22268
BLAST score	287
E value	1.0e-160
Match length	394
% identity	96
NCBI Description	Maize (strain E41) mRNA for cell wall glycoprotein (partial) >gi_168458_gb_M36914_MZECWAC Z.mays cell wall protein mRNA, 3' end

Seq. No.	258606
Contig ID	151_22.R1011
5'-most EST	uC-zmflmo17186c12b1
Method	BLASTX
NCBI GI	g1170937
BLAST score	664
E value	1.0e-69
Match length	129
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258607
Contig ID	151_23.R1011
5'-most EST	LIB3067-008-Q1-K1-E2
Method	BLASTX
NCBI GI	g3915131
BLAST score	346
E value	3.0e-32
Match length	112
% identity	57
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]

Seq. No.	258608
Contig ID	151_24.R1011
5'-most EST	LIB3150-094-P2-K1-D9

Seq. No.	258609
Contig ID	151_25.R1011
5'-most EST	uC-zmflmo17297f07b1
Method	BLASTN
NCBI GI	g4007864
BLAST score	304
E value	1.0e-170
Match length	644
% identity	32
NCBI Description	Zea mays HRGP gene, AC1503 line

Seq. No.	258610
Contig ID	151_27.R1011
5'-most EST	uC-zmflmo17202a02b1
Method	BLASTX
NCBI GI	g1170937
BLAST score	381
E value	2.0e-36
Match length	71
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258611
Contig ID	151_29.R1011
5'-most EST	LIB3068-042-Q1-K1-F7
Method	BLASTN
NCBI GI	g22091
BLAST score	280
E value	1.0e-156
Match length	389
% identity	94
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258612
Contig ID	151_30.R1011
5'-most EST	zla700380237.h1

Seq. No.	258613
Contig ID	151_31.R1011
5'-most EST	uC-zmflb73120h01b1
Method	BLASTN
NCBI GI	g22091
BLAST score	360
E value	0.0e+00
Match length	830
% identity	30
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258614
Contig ID	151_34.R1011
5'-most EST	uC-zmflb73413e11a1
Method	BLASTN
NCBI GI	g22091

BLAST score	268
E value	1.0e-149
Match length	440
% identity	94
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258615
Contig ID	151_38.R1011
5'-most EST	tzu700206801.h1
Method	BLASTX
NCBI GI	g1495251
BLAST score	814
E value	3.0e-87
Match length	230
% identity	64
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258616
Contig ID	151_39.R1011
5'-most EST	LIB3180-019-P2-M1-B12
Method	BLASTX
NCBI GI	g1495251
BLAST score	463
E value	3.0e-46
Match length	106
% identity	81
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258617
Contig ID	151_40.R1011
5'-most EST	LIB3137-039-Q1-K1-G5
Method	BLASTX
NCBI GI	g1170937
BLAST score	445
E value	3.0e-44
Match length	87
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258618
Contig ID	151_41.R1011
5'-most EST	uC-zmrob73055h06b1
Method	BLASTX
NCBI GI	g1495251
BLAST score	272
E value	7.0e-30
Match length	83
% identity	82
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258619
Contig ID	151_43.R1011
5'-most EST	uC-zmroteosinte031f03b1
Method	BLASTX

NCBI GI	g1495251
BLAST score	632
E value	1.0e-102
Match length	258
% identity	71
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258620
Contig ID	151_44.R1011
5'-most EST	uC-zmflmo17042h02b1
Method	BLASTN
NCBI GI	g22091
BLAST score	311
E value	1.0e-175
Match length	446
% identity	94
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258621
Contig ID	151_49.R1011
5'-most EST	nbm700464838.h1

Seq. No.	258622
Contig ID	151_52.R1011
5'-most EST	LIB3078-037-Q1-K1-C6
Method	BLASTX
NCBI GI	g1495251
BLAST score	238
E value	1.0e-19
Match length	121
% identity	50
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	258623
Contig ID	151_53.R1011
5'-most EST	xyt700343661.h1
Method	BLASTX
NCBI GI	g1170937
BLAST score	487
E value	6.0e-49
Match length	125
% identity	82
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	258624
Contig ID	151_63.R1011
5'-most EST	uC-zmflmo17404d03a1
Method	BLASTN
NCBI GI	g22091
BLAST score	230
E value	1.0e-126
Match length	259
% identity	97
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258625
Contig ID	151_64.R1011
5'-most EST	uC-zmflmo17090g08a1
Method	BLASTN
NCBI GI	g22091
BLAST score	262
E value	1.0e-145
Match length	327
% identity	95
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258626
Contig ID	151_67.R1011
5'-most EST	LIB36-017-Q1-E1-E1

Seq. No.	258627
Contig ID	151_71.R1011
5'-most EST	LIB3068-044-Q1-K1-E7
Method	BLASTN
NCBI GI	g22091
BLAST score	148
E value	1.0e-77
Match length	177
% identity	96
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258628
Contig ID	151_81.R1011
5'-most EST	mwy700443224.h2
Method	BLASTX
NCBI GI	g3914019
BLAST score	140
E value	2.0e-14
Match length	61
% identity	72
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2305014 (AF004317) S-adenosyl-L-methionine synthetase homolog [Musa acuminata]

Seq. No.	258629
Contig ID	151_84.R1011
5'-most EST	LIB3180-030-P2-M2-F8

Seq. No.	258630
Contig ID	151_94.R1011
5'-most EST	LIB3069-048-Q1-K1-H1
Method	BLASTN
NCBI GI	g22091
BLAST score	262
E value	1.0e-145
Match length	307
% identity	96
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258631

Contig ID	151_100.R1011
5'-most EST	uC-zmflmo17031c06a1
Method	BLASTN
NCBI GI	g22091
BLAST score	215
E value	1.0e-117
Match length	338
% identity	93
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258632
Contig ID	151_103.R1011
5'-most EST	uC-zmflmo17316h05a1
Method	BLASTN
NCBI GI	g22091
BLAST score	157
E value	4.0e-83
Match length	214
% identity	94
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258633
Contig ID	151_108.R1011
5'-most EST	uC-zmflmo17326d04a1
Method	BLASTN
NCBI GI	g22091
BLAST score	168
E value	1.0e-89
Match length	325
% identity	87
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258634
Contig ID	151_111.R1011
5'-most EST	LIB3068-035-Q1-K1-A3
Method	BLASTN
NCBI GI	g22091
BLAST score	225
E value	1.0e-123
Match length	294
% identity	94
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258635
Contig ID	151_117.R1011
5'-most EST	uC-zmflmo17301b08a1
Method	BLASTN
NCBI GI	g22091
BLAST score	196
E value	1.0e-106
Match length	245
% identity	95
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258636
Contig ID	151_118.R1011
5'-most EST	uC-zmflmo17248b03a1

Method	BLASTN
NCBI GI	g22091
BLAST score	254
E value	1.0e-141
Match length	295
% identity	97
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258637
Contig ID	151_120.R1011
5'-most EST	uC-zmflmo17009f03a1
Method	BLASTN
NCBI GI	g257040
BLAST score	137
E value	2.0e-71
Match length	168
% identity	96
NCBI Description	hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No.	258638
Contig ID	151_126.R1011
5'-most EST	uC-zmflmo17395g06a1
Method	BLASTN
NCBI GI	g4007864
BLAST score	62
E value	2.0e-26
Match length	145
% identity	86
NCBI Description	Zea mays HRGP gene, AC1503 line

Seq. No.	258639
Contig ID	151_127.R1011
5'-most EST	uC-zmflmo17129f02a1
Method	BLASTN
NCBI GI	g22091
BLAST score	184
E value	3.0e-99
Match length	241
% identity	94
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258640
Contig ID	151_130.R1011
5'-most EST	uC-zmflmo17248b06a1
Method	BLASTN
NCBI GI	g22091
BLAST score	88
E value	4.0e-42
Match length	188
% identity	87
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No.	258641
Contig ID	151_136.R1011
5'-most EST	uC-zmflb73411a02a1
Method	BLASTN
NCBI GI	g257040

BLAST score	116
E value	6.0e-59
Match length	139
% identity	96
NCBI Description	hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No.	258642
Contig ID	152_1.R1011
5'-most EST	LIB3066-006-Q1-K1-C7
Method	BLASTX
NCBI GI	g2129753
BLAST score	952
E value	1.0e-103
Match length	237
% identity	76
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	258643
Contig ID	153_1.R1011
5'-most EST	uC-zmf1b73141b02b1
Method	BLASTX
NCBI GI	g2130091
BLAST score	2186
E value	0.0e+00
Match length	439
% identity	96
NCBI Description	aspartate aminotransferase - proso millet >gi_633095_dbj_BAA08106_ (D45076) plastidic aspartate aminotransferase [Panicum miliaceum]

Seq. No.	258644
Contig ID	153_2.R1011
5'-most EST	LIB3150-108-P2-K1-D3
Method	BLASTX
NCBI GI	g2130091
BLAST score	287
E value	1.0e-25
Match length	55
% identity	96
NCBI Description	aspartate aminotransferase - proso millet >gi_633095_dbj_BAA08106_ (D45076) plastidic aspartate aminotransferase [Panicum miliaceum]

Seq. No.	258645
Contig ID	154_1.R1011
5'-most EST	CPR962_700268092_FL
Method	BLASTX
NCBI GI	g2828012
BLAST score	1302
E value	1.0e-160
Match length	281
% identity	100
NCBI Description	(AF036891) starch synthase I precursor [Zea mays]

Seq. No.	258646

Contig ID	155_1.R1011
5'-most EST	CPR9730:2F700213266consensus_FL
Method	BLASTX
NCBI GI	g1946364
BLAST score	1151
E value	1.0e-126
Match length	424
% identity	55
NCBI Description	(U93215) lipase isolog [Arabidopsis thaliana]

Seq. No.	258647
Contig ID	157_1.R1011
5'-most EST	CPR9742consensus_FL
Method	BLASTX
NCBI GI	g2245136
BLAST score	714
E value	2.0e-75
Match length	214
% identity	61
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	258648
Contig ID	158_1.R1011
5'-most EST	CPR17405:2F700282409PROFILIN1.con_FL
Method	BLASTX
NCBI GI	g464466
BLAST score	590
E value	2.0e-60
Match length	204
% identity	63
NCBI Description	PROFILIN 1 >gi_422031_pir__S35796 profilin 1 - maize >gi_313138_emb_CAA51718_ (X73279) profilin 1 [Zea mays]

Seq. No.	258649
Contig ID	158_2.R1011
5'-most EST	LIB3066-018-Q1-K1-A7
Method	BLASTX
NCBI GI	g464466
BLAST score	699
E value	8.0e-74
Match length	131
% identity	100
NCBI Description	PROFILIN 1 >gi_422031_pir__S35796 profilin 1 - maize >gi_313138_emb_CAA51718_ (X73279) profilin 1 [Zea mays]

Seq. No.	258650
Contig ID	158_3.R1011
5'-most EST	LIB3075-054-Q1-K1-B7
Method	BLASTX
NCBI GI	g464466
BLAST score	281
E value	7.0e-25
Match length	54
% identity	100
NCBI Description	PROFILIN 1 >gi_422031_pir__S35796 profilin 1 - maize >gi_313138_emb_CAA51718_ (X73279) profilin 1 [Zea mays]

Seq. No.	258651
Contig ID	158_4.R1011
5'-most EST	LIB3066-010-Q1-K1-H12
Method	BLASTN
NCBI GI	g313137
BLAST score	164
E value	4.0e-87
Match length	272
% identity	95
NCBI Description	Z.mays ZmPRO1 mRNA for profilin

Seq. No.	258652
Contig ID	158_5.R1011
5'-most EST	bdu700382235.h1
Method	BLASTX
NCBI GI	g464466
BLAST score	489
E value	3.0e-49
Match length	102
% identity	92
NCBI Description	PROFILIN 1 >gi_422031_pir__S35796 profilin 1 - maize >gi_313138_emb_CAA51718_ (X73279) profilin 1 [Zea mays]

Seq. No.	258653
Contig ID	159_1.R1011
5'-most EST	LIB3066-027-Q1-K1-D2
Method	BLASTX
NCBI GI	g3901094
BLAST score	857
E value	1.0e-91
Match length	257
% identity	64
NCBI Description	(Z27090) pollen allergen Phl pI [Phleum pratense]

Seq. No.	258654
Contig ID	159_4.R1011
5'-most EST	LIB148-047-Q1-E1-F1
Method	BLASTX
NCBI GI	g1911582
BLAST score	222
E value	4.0e-18
Match length	70
% identity	57
NCBI Description	(S83343) Cyn d 1=major allergen [Cynodon dactylon=Bermuda grass, pollen, Peptide Partial, 246 aa] [Cynodon dactylon]

Seq. No.	258655
Contig ID	159_5.R1011
5'-most EST	LIB3066-032-Q1-K1-D1
Method	BLASTX
NCBI GI	g1171008
BLAST score	268
E value	2.0e-23
Match length	90
% identity	62
NCBI Description	POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)

>gi_629812_pir__S44182 allergen Phl p I - common timothy
>gi_473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum pratense]

Seq. No.	258656
Contig ID	159_6.R1011
5'-most EST	LIB148-066-Q2-E1-C9
Method	BLASTX
NCBI GI	g1911582
BLAST score	175
E value	2.0e-16
Match length	84
% identity	55
NCBI Description	(S83343) Cyn d 1=major allergen [Cynodon dactylon=Bermuda grass, pollen, Peptide Partial, 246 aa] [Cynodon dactylon]

Seq. No.	258657
Contig ID	161_1.R1011
5'-most EST	LIB3066-025-Q1-K1-A9
Method	BLASTX
NCBI GI	g3894172
BLAST score	169
E value	1.0e-23
Match length	150
% identity	42
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	258658
Contig ID	161_2.R1011
5'-most EST	LIB148-066-Q2-E1-H9

Seq. No.	258659
Contig ID	161_3.R1011
5'-most EST	uC-zmf1b73262a01a2
Method	BLASTN
NCBI GI	g2626751
BLAST score	53
E value	7.0e-21
Match length	157
% identity	83
NCBI Description	Triticum aestivum retrotransposon Tar1, partial sequence

Seq. No.	258660
Contig ID	161_4.R1011
5'-most EST	uC-zmflmo17244c09a1
Method	BLASTX
NCBI GI	g3894172
BLAST score	432
E value	2.0e-42
Match length	169
% identity	46
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	258661
Contig ID	163_1.R1011

5'-most EST	RA012A10_700336827_FL
Method	BLASTX
NCBI GI	g4204288
BLAST score	617
E value	4.0e-76
Match length	412
% identity	42
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	258662
Contig ID	165_1.R1011
5'-most EST	ntr700074680.h1
Method	BLASTX
NCBI GI	g3790587
BLAST score	858
E value	7.0e-92
Match length	354
% identity	54
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	258663
Contig ID	165_2.R1011
5'-most EST	LIB3075-032-Q1-K1-A8

Seq. No.	258664
Contig ID	165_3.R1011
5'-most EST	wty700165881.h1
Method	BLASTX
NCBI GI	g3790587
BLAST score	153
E value	3.0e-14
Match length	74
% identity	66
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	258665
Contig ID	165_4.R1011
5'-most EST	nbm700477612.h1
Method	BLASTX
NCBI GI	g3790587
BLAST score	415
E value	1.0e-40
Match length	86
% identity	88
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	258666
Contig ID	166_1.R1011
5'-most EST	uC-zmflMo17092d01b1
Method	BLASTX
NCBI GI	g862650
BLAST score	506
E value	7.0e-51

Match length	198
% identity	53
NCBI Description	(U20193) MADS-box protein AGL12 [Arabidopsis thaliana]

Seq. No.	258667
Contig ID	166_2.R1011
5'-most EST	uC-zmflb73186e10b1
Method	BLASTX
NCBI GI	g862650
BLAST score	296
E value	1.0e-26
Match length	76
% identity	68
NCBI Description	(U20193) MADS-box protein AGL12 [Arabidopsis thaliana]

Seq. No.	258668
Contig ID	166_3.R1011
5'-most EST	uC-zmroteosinte085a11b1
Method	BLASTX
NCBI GI	g862650
BLAST score	297
E value	8.0e-27
Match length	76
% identity	70
NCBI Description	(U20193) MADS-box protein AGL12 [Arabidopsis thaliana]

Seq. No.	258669
Contig ID	166_4.R1011
5'-most EST	uC-zmflb73097b01a2

Seq. No.	258670
Contig ID	166_5.R1011
5'-most EST	uC-zmromo17107e01a1

Seq. No.	258671
Contig ID	167_1.R1011
5'-most EST	clt700044153.f1
Method	BLASTX
NCBI GI	g1553133
BLAST score	179
E value	2.0e-12
Match length	192
% identity	12
NCBI Description	(U64722) actin-fragmin kinase [Physarum polycephalum]

Seq. No.	258672
Contig ID	167_4.R1011
5'-most EST	nwy700444883.h1

Seq. No.	258673
Contig ID	168_1.R1011
5'-most EST	RA012B12_700347284_FL
Method	BLASTX
NCBI GI	g2865394
BLAST score	889
E value	1.0e-95
Match length	301

% identity	60
NCBI Description	(AF036949) basic leucine zipper protein [Zea mays]

Seq. No.	258674
Contig ID	171_1.R1011
5'-most EST	RA012B6_700344331_FL
Method	BLASTX
NCBI GI	g1304266
BLAST score	323
E value	1.0e-29
Match length	117
% identity	61
NCBI Description	(D64051) HALF-1 [Triticum aestivum]

Seq. No.	258675
Contig ID	173_1.R1011
5'-most EST	uwc700152704.h1
Method	BLASTX
NCBI GI	g3738230
BLAST score	273
E value	2.0e-23
Match length	223
% identity	32
NCBI Description	(AB007790) DREB2A [Arabidopsis thaliana] >gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis thaliana]

Seq. No.	258676
Contig ID	174_1.R1011
5'-most EST	LIB3069-023-Q1-K1-H5
Method	BLASTX
NCBI GI	g1753085
BLAST score	325
E value	8.0e-30
Match length	157
% identity	53
NCBI Description	(U25283) leucine zipper protein [Oryza sativa]

Seq. No.	258677
Contig ID	174_2.R1011
5'-most EST	LIB3067-042-Q1-K1-B12
Method	BLASTX
NCBI GI	g1753085
BLAST score	249
E value	9.0e-24
Match length	93
% identity	65
NCBI Description	(U25283) leucine zipper protein [Oryza sativa]

Seq. No.	258678
Contig ID	175_1.R1011
5'-most EST	RA012C7_700350520_FL
Method	BLASTX
NCBI GI	g2145356
BLAST score	3031
E value	0.0e+00
Match length	789

% identity	75
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	258679
Contig ID	175_2.R1011
5'-most EST	LIB3279-008-P1-K1-H7
Method	BLASTX
NCBI GI	g2145356
BLAST score	212
E value	6.0e-17
Match length	49
% identity	76
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	258680
Contig ID	175_6.R1011
5'-most EST	nbm700471323.h1
Method	BLASTX
NCBI GI	g2145358
BLAST score	342
E value	2.0e-45
Match length	127
% identity	77
NCBI Description	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No.	258681
Contig ID	176_1.R1011
5'-most EST	uC-zmflb73001e04b1
Method	BLASTX
NCBI GI	g2911067
BLAST score	1432
E value	0.0e+00
Match length	641
% identity	76
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	258682
Contig ID	176_2.R1011
5'-most EST	xyt700344948.h1
Method	BLASTX
NCBI GI	g2911067
BLAST score	500
E value	2.0e-50
Match length	123
% identity	77
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	258683
Contig ID	178_1.R1011
5'-most EST	RT001A12FL_700076615_FL

Seq. No.	258684
Contig ID	179_1.R1011

5'-most EST	LIB3151-026-Q1-K1-D12
Seq. No.	258685
Contig ID	180_1.R1011
5'-most EST	LIB3152-016-P1-K1-B2
Method	BLASTX
NCBI GI	g2224899
BLAST score	281
E value	2.0e-24
Match length	195
% identity	38
NCBI Description	(U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]
Seq. No.	258686
Contig ID	180_2.R1011
5'-most EST	LIB3151-023-Q1-K1-F1
Method	BLASTX
NCBI GI	g2224901
BLAST score	217
E value	2.0e-17
Match length	68
% identity	60
NCBI Description	(U67134) PcMYB1 protein [Petroselinum crispum]
Seq. No.	258687
Contig ID	181_1.R1011
5'-most EST	xsy700209975.h1
Method	BLASTX
NCBI GI	g1705594
BLAST score	238
E value	2.0e-19
Match length	220
% identity	33
NCBI Description	PEROXISOME ASSEMBLY PROTEIN CAR1 (PEROXIN-2) >gi_2133320_pir__A56730 car1 protein - Podospora anserina >gi_1360119_emb_CAA60739_ (X87329) peroxisome assembly factor [Podospora anserina]
Seq. No.	258688
Contig ID	182_1.R1011
5'-most EST	RT001E1_700023190_FL
Method	BLASTX
NCBI GI	g1432058
BLAST score	492
E value	4.0e-49
Match length	236
% identity	48
NCBI Description	(U58540) WRKY2 [Petroselinum crispum]
Seq. No.	258689
Contig ID	182_2.R1011
5'-most EST	gwl700613365.h1
Method	BLASTX
NCBI GI	g1432058
BLAST score	281
E value	2.0e-24
Match length	104

% identity	61
NCBI Description	(U58540) WRKY2 [Petroselinum crispum]

Seq. No.	258690
Contig ID	182_3.R1011
5'-most EST	uC-zmflb73177e04b1

Seq. No.	258691
Contig ID	183_1.R1011
5'-most EST	RT001E2_700025985_FL

Seq. No.	258692
Contig ID	184_1.R1011
5'-most EST	RT001E3FL_700026214_FL
Method	BLASTX
NCBI GI	g122772
BLAST score	1211
E value	1.0e-133
Match length	329
% identity	76
NCBI Description	TRANSCRIPTION FACTOR HBP-1B >gi_100809_pir__S15347 transcription factor HBP-1b - wheat >gi_21635_emb_CAA40102_ (X56782) HBP-1b [Triticum aestivum]

Seq. No.	258693
Contig ID	185_1.R1011
5'-most EST	RT001F6_700028403_FL
Method	BLASTX
NCBI GI	g1168546
BLAST score	298
E value	2.0e-26
Match length	151
% identity	49
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-5 (HD-ZIP PROTEIN ATHB-5) >gi_629504_pir__S47135 homeotic protein Athb-5 - Arabidopsis thaliana >gi_499160_emb_CAA47426_ (X67033) Athb-5 [Arabidopsis thaliana]

Seq. No.	258694
Contig ID	186_1.R1011
5'-most EST	RT001G10FL_700104561_FL
Method	BLASTX
NCBI GI	g2194132
BLAST score	833
E value	4.0e-89
Match length	375
% identity	50
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	258695
Contig ID	187_1.R1011
5'-most EST	RT001G11_700106005_FL
Method	BLASTX
NCBI GI	g3047106
BLAST score	1397
E value	1.0e-155
Match length	410

% identity	68
NCBI Description	(AF058919) Arabidopsis thaliana homeodomain protein AHDP (SP:P93041) [Arabidopsis thaliana]
Seq. No.	258696
Contig ID	188_1.R1011
5'-most EST	RT001G1_700030417_FL
Seq. No.	258697
Contig ID	189_1.R1011
5'-most EST	fC-zmst1700333259f1
Method	BLASTX
NCBI GI	g1899060
BLAST score	1576
E value	1.0e-176
Match length	328
% identity	91
NCBI Description	(U79669) endosperm C-24 sterol methyltransferase [Zea mays]
Seq. No.	258698
Contig ID	189_2.R1011
5'-most EST	uwc700155621.h1
Method	BLASTX
NCBI GI	g1899060
BLAST score	184
E value	1.0e-26
Match length	81
% identity	80
NCBI Description	(U79669) endosperm C-24 sterol methyltransferase [Zea mays]
Seq. No.	258699
Contig ID	190_1.R1011
5'-most EST	gwl700612536.h1
Method	BLASTX
NCBI GI	g3168840
BLAST score	284
E value	8.0e-25
Match length	65
% identity	82
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]
Seq. No.	258700
Contig ID	191_1.R1011
5'-most EST	RT001G7_700099947_FL
Method	BLASTX
NCBI GI	g551535
BLAST score	263
E value	2.0e-22
Match length	175
% identity	29
NCBI Description	(U14134) transcription factor IIIA [Homo sapiens]
Seq. No.	258701
Contig ID	192_1.R1011
5'-most EST	RT001H1_700086694_FL
Method	BLASTX
NCBI GI	g2642154

BLAST score	282
E value	1.0e-24
Match length	135
% identity	50
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana]

Seq. No.	258702
Contig ID	193_1.R1011
5'-most EST	hbs701180711.h1
Method	BLASTX
NCBI GI	g1747310
BLAST score	538
E value	2.0e-54
Match length	212
% identity	49
NCBI Description	(D58424) Myb-like DNA binding protein [Arabidopsis thaliana]

Seq. No.	258703
Contig ID	193_2.R1011
5'-most EST	kem700611496.h1

Seq. No.	258704
Contig ID	194_1.R1011
5'-most EST	RT001H5_700088489_FL
Method	BLASTX
NCBI GI	g2317905
BLAST score	285
E value	7.0e-25
Match length	325
% identity	26
NCBI Description	(U89959) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	258705
Contig ID	195_2.R1011
5'-most EST	LIB3150-116-P2-K1-F12
Method	BLASTX
NCBI GI	g2146866
BLAST score	152
E value	2.0e-09
Match length	169
% identity	25
NCBI Description	gene C35D10.10 protein - Caenorhabditis elegans >gi_687889 (U21324) weak similarity to aa 31-55 of A. thaliana thioredoxine [Caenorhabditis elegans]

Seq. No.	258706
Contig ID	196_1.R1011
5'-most EST	LIB3156-016-Q1-K1-B6
Method	BLASTX
NCBI GI	g1345644
BLAST score	1830
E value	0.0e+00
Match length	473
% identity	72

NCBI Description	CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446_emb_CAA62082_ (X90458) cytochrome p450 [Arabidopsis thaliana]
Seq. No.	258707
Contig ID	204_1.R1011
5'-most EST	uC-zmflb73272h04b1
Method	BLASTX
NCBI GI	g3142291
BLAST score	298
E value	2.0e-26
Match length	136
% identity	45
NCBI Description	(AC002411) Contains similarity to adenylate cyclase gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes from this gene. [Arabidopsis thaliana]
Seq. No.	258708
Contig ID	205_1.R1011
5'-most EST	LIB3066-042-Q1-K1-D9
Method	BLASTX
NCBI GI	g1399277
BLAST score	1439
E value	1.0e-160
Match length	477
% identity	59
NCBI Description	(U31836) calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana]
Seq. No.	258709
Contig ID	205_2.R1011
5'-most EST	LIB148-040-Q1-E1-B8
Method	BLASTX
NCBI GI	g1871195
BLAST score	152
E value	3.0e-09
Match length	56
% identity	55
NCBI Description	(U90439) Ca++ dependent protein kinase isolog [Arabidopsis thaliana] >gi_2335093 (AC002339) putative calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.	258710
Contig ID	206_1.R1011
5'-most EST	fC-gmst700662785_FL
Method	BLASTX
NCBI GI	g2462749
BLAST score	256
E value	6.0e-22
Match length	85
% identity	66
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
Seq. No.	258711
Contig ID	207_1.R1011
5'-most EST	fC-zmfl700354473f2
Method	BLASTX

NCBI GI	g2832691
BLAST score	695
E value	7.0e-92
Match length	328
% identity	52
NCBI Description	(AL021713) polygalacturonase-like protein [Arabidopsis thaliana]

Seq. No.	258712
Contig ID	208_1.R1011
5'-most EST	uC-zmflmo17076d02a1
Method	BLASTX
NCBI GI	g1155255
BLAST score	499
E value	4.0e-50
Match length	242
% identity	42
NCBI Description	(U39228) beta-glucosidase [Prunus avium]

Seq. No.	258713
Contig ID	208_2.R1011
5'-most EST	uC-zmroteosinte106g09b2
Method	BLASTX
NCBI GI	g1155255
BLAST score	235
E value	8.0e-32
Match length	133
% identity	52
NCBI Description	(U39228) beta-glucosidase [Prunus avium]

Seq. No.	258714
Contig ID	209_1.R1011
5'-most EST	fC-zmfl700338026_FL
Method	BLASTX
NCBI GI	g2642640
BLAST score	451
E value	1.0e-44
Match length	111
% identity	77
NCBI Description	(AF032473) ADP-glucose pyrophosphorylase large subunit 2 [Citrullus lanatus]

Seq. No.	258715
Contig ID	210_1.R1011
5'-most EST	fC-zmfl700338726_FL

Seq. No.	258716
Contig ID	211_1.R1011
5'-most EST	LIB3088-046-Q1-K1-F12
Method	BLASTX
NCBI GI	g231707
BLAST score	730
E value	2.0e-77
Match length	154
% identity	89
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 2 >gi_100668_pir__S22441 protein kinase (EC 2.7.1.37) cdc2

	homolog 2 - rice >gi_20345_emb_CAA42923_ (X60375) Rcdc2-2 [Oryza sativa] >gi_228925_prf__1814443B cdc2 protein:ISOTYPE=cdc2Os-2 [Oryza sativa]
Seq. No.	258717
Contig ID	212_1.R1011
5'-most EST	nbm700478009.h1
Method	BLASTX
NCBI GI	g3800878
BLAST score	1799
E value	0.0e+00
Match length	494
% identity	70
NCBI Description	(AF096281) threonine dehydratase/deaminase [Arabidopsis thaliana]
Seq. No.	258718
Contig ID	212_2.R1011
5'-most EST	uC-zmrob73002f07a1
Seq. No.	258719
Contig ID	212_3.R1011
5'-most EST	uC-zmflb73304f01a1
Seq. No.	258720
Contig ID	213_1.R1011
5'-most EST	ymt700220010.h1
Method	BLASTX
NCBI GI	g3790587
BLAST score	250
E value	6.0e-21
Match length	59
% identity	75
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]
Seq. No.	258721
Contig ID	214_1.R1011
5'-most EST	fC-zmfl700341881_FL
Method	BLASTX
NCBI GI	g4154279
BLAST score	534
E value	2.0e-54
Match length	145
% identity	65
NCBI Description	(AF082346) C13 endopeptidase NP1 precursor [Hordeum vulgare]
Seq. No.	258722
Contig ID	215_1.R1011
5'-most EST	LIB3150-019-Q1-N1-H3
Method	BLASTX
NCBI GI	g4582459
BLAST score	516
E value	5.0e-52
Match length	226
% identity	50

NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	258723
Contig ID	215_2.R1011
5'-most EST	uC-zmflmo17016f02a1

Seq. No.	258724
Contig ID	216_1.R1011
5'-most EST	fC-zmfl700342726_FL
Method	BLASTX
NCBI GI	g3021268
BLAST score	197
E value	5.0e-15
Match length	112
% identity	39
NCBI Description	(AL022347) putative protein [Arabidopsis thaliana]

Seq. No.	258725
Contig ID	217_1.R1011
5'-most EST	fC-zmfl700342745_FL
Method	BLASTX
NCBI GI	g2465923
BLAST score	627
E value	3.0e-65
Match length	248
% identity	54
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	258726
Contig ID	218_1.R1011
5'-most EST	kem700612112.h1
Method	BLASTX
NCBI GI	g3309066
BLAST score	2208
E value	0.0e+00
Match length	429
% identity	97
NCBI Description	(AF073488) bifunctional dihydrofolate reductase-thymidylate synthase [Zea mays]

Seq. No.	258727
Contig ID	218_2.R1011
5'-most EST	LIB3067-002-Q1-K1-D10
Method	BLASTX
NCBI GI	g3309066
BLAST score	354
E value	2.0e-33
Match length	68
% identity	97
NCBI Description	(AF073488) bifunctional dihydrofolate reductase-thymidylate synthase [Zea mays]

Seq. No.	258728
Contig ID	219_1.R1011
5'-most EST	uC-zmflb73245e04b2

Method	BLASTX
NCBI GI	g3047123
BLAST score	415
E value	3.0e-40
Match length	169
% identity	48
NCBI Description	(AF058919) similar to the family of glycosyl hydrolases [Arabidopsis thaliana]

Seq. No.	258729
Contig ID	219_2.R1011
5'-most EST	LIB3067-030-Q1-K1-C3
Method	BLASTX
NCBI GI	g3047123
BLAST score	727
E value	4.0e-77
Match length	204
% identity	62
NCBI Description	(AF058919) similar to the family of glycosyl hydrolases [Arabidopsis thaliana]

Seq. No.	258730
Contig ID	220_1.R1011
5'-most EST	LIB3137-003-Q1-K1-F4
Method	BLASTX
NCBI GI	g3176669
BLAST score	487
E value	1.0e-48
Match length	213
% identity	48
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.	258731
Contig ID	221_1.R1011
5'-most EST	fC-zmf1700343886_FL
Method	BLASTX
NCBI GI	g4580398
BLAST score	746
E value	6.0e-79
Match length	198
% identity	71
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No.	258732
Contig ID	222_1.R1011
5'-most EST	fC-zmf1700344343_FL
Method	BLASTX
NCBI GI	g3482921
BLAST score	264
E value	2.0e-22
Match length	79
% identity	62
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No.	258733
Contig ID	223_1.R1011

5'-most EST	fC-zmf1700344346:_FL
Seq. No.	258734
Contig ID	224_1.R1011
5'-most EST	LIB3061-007-Q1-K1-F5
Method	BLASTX
NCBI GI	g1076318
BLAST score	1110
E value	1.0e-121
Match length	332
% identity	66
NCBI Description	dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) precursor - Arabidopsis thaliana (fragment) >gi_559395_emb_CAA86300_ (Z46230) dihydrolipoamide acetyltransferase (E2) subunit of PDC [Arabidopsis thaliana]
Seq. No.	258735
Contig ID	225_1.R1011
5'-most EST	uwc700153592.h1
Method	BLASTX
NCBI GI	g1076486
BLAST score	628
E value	4.0e-65
Match length	215
% identity	55
NCBI Description	cim1 protein - soybean >gi_555616 (U03860) cytokinin induced message [Glycine max]
Seq. No.	258736
Contig ID	226_1.R1011
5'-most EST	LIB83-005-Q1-E1-C1
Method	BLASTX
NCBI GI	g3122357
BLAST score	747
E value	3.0e-79
Match length	224
% identity	63
NCBI Description	PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS PROTEIN B) >gi_2494127 (AC002376) Contains similarity to Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis thaliana]
Seq. No.	258737
Contig ID	227_1.R1011
5'-most EST	LIB143-064-Q1-E1-B9
Method	BLASTX
NCBI GI	g3786005
BLAST score	1542
E value	1.0e-172
Match length	365
% identity	80
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]
Seq. No.	258738
Contig ID	227_2.R1011

5'-most EST	ymt700224159.h1
Method	BLASTX
NCBI GI	g3786005
BLAST score	462
E value	2.0e-46
Match length	100
% identity	87
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	258739
Contig ID	228_1.R1011
5'-most EST	fC-zmle700445521a1
Method	BLASTX
NCBI GI	g1708236
BLAST score	756
E value	3.0e-80
Match length	236
% identity	63
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	258740
Contig ID	228_2.R1011
5'-most EST	LIB3075-014-Q1-K1-F9
Method	BLASTX
NCBI GI	g1708236
BLAST score	257
E value	5.0e-22
Match length	86
% identity	60
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	258741
Contig ID	228_3.R1011
5'-most EST	LIB3180-048-P2-C12
Method	BLASTX
NCBI GI	g4098521
BLAST score	1422
E value	1.0e-158
Match length	343
% identity	77
NCBI Description	(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi_4098523 (U79161) HMG-CoA synthase [Arabidopsis

thaliana]

Seq. No.	258742
Contig ID	228_4.R1011
5'-most EST	LIB3136-016-Q1-K1-A12

Seq. No.	258743
Contig ID	229_1.R1011
5'-most EST	fC-zmfl700352002_FL
Method	BLASTX
NCBI GI	g585593
BLAST score	220
E value	3.0e-17
Match length	188
% identity	27
NCBI Description	NUCLEAR PORE GLYCOPROTEIN P62 (NUCLEOPORIN P62) >gi_432654_emb_CAA41411_ (X58521) nucleoporin p62 [Homo sapiens]

Seq. No.	258744
Contig ID	230_1.R1011
5'-most EST	fC-zmfl700345914_FL
Method	BLASTN
NCBI GI	g2911359
BLAST score	118
E value	2.0e-59
Match length	367
% identity	89
NCBI Description	Zea mays NADPH HC toxin reductase (hm1) gene, hm1-Pr allele, complete cds

Seq. No.	258745
Contig ID	231_1.R1011
5'-most EST	LIB3062-039-Q1-K1-F3

Seq. No.	258746
Contig ID	232_1.R1011
5'-most EST	LIB3075-008-Q1-K1-A5
Method	BLASTX
NCBI GI	g2498077
BLAST score	761
E value	6.0e-81
Match length	149
% identity	98
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase [Saccharum officinarum]

Seq. No.	258747
Contig ID	233_1.R1011
5'-most EST	uC-zmflb73158e10b2
Method	BLASTX
NCBI GI	g3201626
BLAST score	1204
E value	1.0e-132
Match length	287
% identity	78

NCBI Description	(AC004669) putative protein kinase MAP3K [Arabidopsis thaliana]
Seq. No.	258748
Contig ID	234_1.R1011
5'-most EST	fC-zmfl700348029:_FL
Seq. No.	258749
Contig ID	234_3.R1011
5'-most EST	hvj700621656.h1
Seq. No.	258750
Contig ID	235_1.R1011
5'-most EST	uC-zmflb73091c01b2
Method	BLASTX
NCBI GI	g267196
BLAST score	2070
E value	0.0e+00
Match length	575
% identity	68
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_66574_pir__YUPOY ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - potato >gi_21471_emb_CAA41359_ (X58453) glycogen (starch) synthase [Solanum tuberosum]
Seq. No.	258751
Contig ID	235_2.R1011
5'-most EST	uC-zmflb73143a08b1
Method	BLASTX
NCBI GI	g3688123
BLAST score	423
E value	8.0e-69
Match length	244
% identity	59
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]
Seq. No.	258752
Contig ID	235_3.R1011
5'-most EST	fC-zmst700454550f1
Seq. No.	258753
Contig ID	235_4.R1011
5'-most EST	uC-zmflb73100g10b1
Method	BLASTX
NCBI GI	g267196
BLAST score	223
E value	6.0e-18
Match length	54
% identity	78
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_66574_pir__YUPOY ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - potato >gi_21471_emb_CAA41359_ (X58453) glycogen (starch) synthase [Solanum tuberosum]
Seq. No.	258754
Contig ID	236_1.R1011

5'-most EST	fC-zmle700422033_FL
Seq. No.	258755
Contig ID	237_1.R1011
5'-most EST	fC-zmfl700349253_FL
Method	BLASTX
NCBI GI	g126334
BLAST score	257
E value	1.0e-21
Match length	277
% identity	32
NCBI Description	LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE) >gi_79925_pir__A24075 lipase precursor - Staphylococcus hyicus >gi_47136_emb_CAA26602_ (X02844) precursor [Staphylococcus hyicus]
Seq. No.	258756
Contig ID	238_1.R1011
5'-most EST	fC-zmfl700350038_FL
Method	BLASTX
NCBI GI	g1495802
BLAST score	2024
E value	0.0e+00
Match length	626
% identity	60
NCBI Description	(X96405) 13-lipoxygenase [Solanum tuberosum]
Seq. No.	258757
Contig ID	238_2.R1011
5'-most EST	uC-zmflMo17009h06b1
Method	BLASTX
NCBI GI	g1495802
BLAST score	536
E value	2.0e-80
Match length	280
% identity	56
NCBI Description	(X96405) 13-lipoxygenase [Solanum tuberosum]
Seq. No.	258758
Contig ID	238_3.R1011
5'-most EST	LIB189-001-Q1-E1-G4
Method	BLASTX
NCBI GI	g2826842
BLAST score	349
E value	8.0e-33
Match length	106
% identity	61
NCBI Description	(AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
Seq. No.	258759
Contig ID	238_4.R1011
5'-most EST	LIB3060-028-Q1-K1-F9
Seq. No.	258760
Contig ID	238_5.R1011
5'-most EST	pwr700452561.h1
Method	BLASTX

NCBI GI	g2826842
BLAST score	365
E value	9.0e-35
Match length	137
% identity	55
NCBI Description	(AJ002236) loxc homologue [Lycopersicon pimpinellifolium]

Seq. No.	258761
Contig ID	238_6.R1011
5'-most EST	uC-zmflmo17420g06a1
Method	BLASTX
NCBI GI	g626032
BLAST score	429
E value	2.0e-42
Match length	121
% identity	65
NCBI Description	lipoxygenase L-2 - rice

Seq. No.	258762
Contig ID	239_1.R1011
5'-most EST	fC-zmfl700351139_FL
Method	BLASTX
NCBI GI	g2827715
BLAST score	817
E value	3.0e-87
Match length	237
% identity	69
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	258763
Contig ID	240_1.R1011
5'-most EST	fC-zmfl700351266_FL
Method	BLASTX
NCBI GI	g4263791
BLAST score	476
E value	1.0e-47
Match length	147
% identity	59
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	258764
Contig ID	240_2.R1011
5'-most EST	uC-zmflb73233h08a1

Seq. No.	258765
Contig ID	241_1.R1011
5'-most EST	uC-zmflb73013h07b1
Method	BLASTX
NCBI GI	g1154889
BLAST score	2010
E value	0.0e+00
Match length	566
% identity	74
NCBI Description	(Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza sativa] >gi_1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA

reductase [Oryza sativa]

Seq. No.	258766
Contig ID	241_2.R1011
5'-most EST	uC-zmflm017209d08b1
Method	BLASTX
NCBI GI	g1154889
BLAST score	178
E value	1.0e-12
Match length	58
% identity	64
NCBI Description	(Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza sativa] >gi_1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA reductase [Oryza sativa]

Seq. No.	258767
Contig ID	241_3.R1011
5'-most EST	uC-zmflm017209f12b1
Method	BLASTX
NCBI GI	g1154889
BLAST score	1067
E value	1.0e-117
Match length	237
% identity	87
NCBI Description	(Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza sativa] >gi_1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA reductase [Oryza sativa]

Seq. No.	258768
Contig ID	241_4.R1011
5'-most EST	uC-zmroteosinte064b12b1

Seq. No.	258769
Contig ID	242_1.R1011
5'-most EST	wty700169504.h1
Method	BLASTX
NCBI GI	g520582
BLAST score	1292
E value	1.0e-143
Match length	342
% identity	69
NCBI Description	(D37796) Ids3 [Hordeum vulgare]

Seq. No.	258770
Contig ID	243_1.R1011
5'-most EST	LIB3118-003-Q1-K1-F3
Method	BLASTX
NCBI GI	g1911822
BLAST score	476
E value	2.0e-47
Match length	217
% identity	46
NCBI Description	(S83425) glycosylasparaginase alpha beta {EC 3.5.1.26} [Spodoptera frugiperda, Sf9, Peptide, 320 aa] [Spodoptera frugiperda]

Seq. No. 258771

Contig ID	243_3.R1011
5'-most EST	uC-zmflb73250e07a2
Seq. No.	258772
Contig ID	245_1.R1011
5'-most EST	uC-zmflmo17022h09b1
Seq. No.	258773
Contig ID	245_2.R1011
5'-most EST	uC-zmflb73213d03b1
Method	BLASTX
NCBI GI	g3879734
BLAST score	259
E value	6.0e-22
Match length	230
% identity	33
NCBI Description	(Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727
Seq. No.	258774
Contig ID	245_3.R1011
5'-most EST	uC-zmroteosinte074c09b1
Seq. No.	258775
Contig ID	245_4.R1011
5'-most EST	LIB3067-026-Q1-K1-D3
Seq. No.	258776
Contig ID	245_5.R1011
5'-most EST	rvl700457670.h1
Seq. No.	258777
Contig ID	245_6.R1011
5'-most EST	uC-zmflmo17204h02b1
Seq. No.	258778
Contig ID	245_8.R1011
5'-most EST	pmx700086066.h1
Seq. No.	258779
Contig ID	245_11.R1011
5'-most EST	uC-zmflb73130h10a1
Method	BLASTX
NCBI GI	g3879734
BLAST score	149
E value	9.0e-10
Match length	48
% identity	62
NCBI Description	(Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727
Seq. No.	258780
Contig ID	245_12.R1011

5'-most EST	nwy700447484.h1
Seq. No.	258781
Contig ID	247_1.R1011
5'-most EST	wen700336979.h1
Method	BLASTX
NCBI GI	g4544432
BLAST score	1381
E value	1.0e-153
Match length	395
% identity	69
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]
Seq. No.	258782
Contig ID	247_2.R1011
5'-most EST	uC-zmflmo17375b08a1
Seq. No.	258783
Contig ID	248_1.R1011
5'-most EST	fC-zmfl700352293_FL
Method	BLASTX
NCBI GI	g127112
BLAST score	450
E value	4.0e-44
Match length	175
% identity	51
NCBI Description	MAK16 PROTEIN >gi_73269_pir__BVBYK6 MAK16 protein - yeast (Saccharomyces cerevisiae) >gi_171880 (J03852) MAK16 protein [Saccharomyces cerevisiae] >gi_595561 (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]
Seq. No.	258784
Contig ID	249_1.R1011
5'-most EST	wty700169932.h1
Method	BLASTX
NCBI GI	g629561
BLAST score	615
E value	1.0e-63
Match length	348
% identity	42
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]
Seq. No.	258785
Contig ID	249_2.R1011
5'-most EST	gct701176519.h1
Method	BLASTX
NCBI GI	g4454018
BLAST score	389
E value	2.0e-37
Match length	226
% identity	43
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]
Seq. No.	258786

Contig ID	250_1.R1011
5'-most EST	fC-zmfl700353002_FL
Method	BLASTX
NCBI GI	g2245066
BLAST score	589
E value	2.0e-60
Match length	269
% identity	47
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	258787
Contig ID	251_1.R1011
5'-most EST	LIB3075-023-Q1-K1-E7
Method	BLASTX
NCBI GI	g3355471
BLAST score	851
E value	3.0e-91
Match length	270
% identity	58
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	258788
Contig ID	252_1.R1011
5'-most EST	LIB3137-043-Q1-K1-D7
Method	BLASTX
NCBI GI	g2829275
BLAST score	796
E value	7.0e-85
Match length	237
% identity	67
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	258789
Contig ID	252_2.R1011
5'-most EST	LIB3066-025-Q1-K1-H9
Method	BLASTX
NCBI GI	g2829275
BLAST score	373
E value	1.0e-35
Match length	78
% identity	86
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	258790
Contig ID	252_3.R1011
5'-most EST	uC-zmflmo17192h08b1

Method	BLASTX
NCBI GI	g2829275
BLAST score	225
E value	2.0e-18
Match length	116
% identity	48
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	258791
Contig ID	252_5.R1011
5'-most EST	fC-zmst700619865r1
Method	BLASTX
NCBI GI	g2829275
BLAST score	304
E value	8.0e-28
Match length	64
% identity	88
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	258792
Contig ID	253_1.R1011
5'-most EST	fC-zmfl700353723:_FL
Method	BLASTX
NCBI GI	g169705
BLAST score	831
E value	5.0e-89
Match length	183
% identity	87
NCBI Description	(M64737) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	258793
Contig ID	253_2.R1011
5'-most EST	uC-zmflmo17313a07b1
Method	BLASTX
NCBI GI	g2497539
BLAST score	1411
E value	1.0e-157
Match length	311
% identity	88
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	258794
Contig ID	254_1.R1011
5'-most EST	fC-zmfl700354490_FL
Method	BLASTX
NCBI GI	g1899175

BLAST score	600
E value	7.0e-62
Match length	179
% identity	68
NCBI Description	(U90262) calcium-dependent calmodulin-independent protein kinase CDPK [Cucurbita pepo]

Seq. No.	258795
Contig ID	255_1.R1011
5'-most EST	LIB3150-032-Q1-N1-C6
Method	BLASTX
NCBI GI	g1587206
BLAST score	2454
E value	0.0e+00
Match length	533
% identity	89
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	258796
Contig ID	255_2.R1011
5'-most EST	LIB3150-027-Q1-N1-D6
Method	BLASTX
NCBI GI	g1587206
BLAST score	282
E value	4.0e-25
Match length	59
% identity	88
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	258797
Contig ID	255_3.R1011
5'-most EST	uC-zmroteosinte001a02b1
Method	BLASTX
NCBI GI	g1587206
BLAST score	374
E value	6.0e-36
Match length	82
% identity	85
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	258798
Contig ID	255_4.R1011
5'-most EST	ymt700220262.h1
Method	BLASTX
NCBI GI	g1587206
BLAST score	488
E value	3.0e-49
Match length	107
% identity	93
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	258799
Contig ID	255_5.R1011
5'-most EST	cat700017202.r1

Seq. No.	258800
Contig ID	256_1.R1011

5'-most EST	LIB3066-030-Q1-K1-D3
Method	BLASTX
NCBI GI	g548493
BLAST score	1170
E value	1.0e-128
Match length	414
% identity	55
NCBI Description	EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_629854_pir__S30067 polygalacturonase - maize >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea mays]

Seq. No.	258801
Contig ID	256_2.R1011
5'-most EST	uC-zmflmo17218b05a1
Method	BLASTX
NCBI GI	g3193292
BLAST score	294
E value	9.0e-36
Match length	136
% identity	63
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	258802
Contig ID	256_3.R1011
5'-most EST	LIB148-050-Q1-E1-B11
Method	BLASTX
NCBI GI	g22422
BLAST score	301
E value	2.0e-27
Match length	95
% identity	60
NCBI Description	(X57743) polygalacturonase [Zea mays]

Seq. No.	258803
Contig ID	256_5.R1011
5'-most EST	LIB148-028-Q1-E1-B10
Method	BLASTX
NCBI GI	g548493
BLAST score	213
E value	4.0e-17
Match length	116
% identity	41
NCBI Description	EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_629854_pir__S30067 polygalacturonase - maize >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea mays]

Seq. No.	258804
Contig ID	257_1.R1011
5'-most EST	fC-zmf1700354921_FL
Method	BLASTN
NCBI GI	g429006

BLAST score 39
E value 3.0e-12
Match length 95
% identity 85
NCBI Description Rice mRNA for MCM3 (gene name SS300), partial cds

Seq. No. 258805
Contig ID 257_2.R1011
5'-most EST yyf700352534.h1

Seq. No. 258806
Contig ID 257_3.R1011
5'-most EST uC-zmflMo17005g11b1

Seq. No. 258807
Contig ID 257_4.R1011
5'-most EST LIB3137-020-Q1-K1-D2
Method BLASTN
NCBI GI g429006
BLAST score 39
E value 2.0e-12
Match length 95
% identity 85
NCBI Description Rice mRNA for MCM3 (gene name SS300), partial cds

Seq. No. 258808
Contig ID 257_5.R1011
5'-most EST xyt700345654.h1

Seq. No. 258809
Contig ID 258_1.R1011
5'-most EST pmx700091042.h1
Method BLASTX
NCBI GI g4107009
BLAST score 2217
E value 0.0e+00
Match length 499
% identity 86
NCBI Description (D82039) OSK1 [Oryza sativa]

Seq. No. 258810
Contig ID 258_2.R1011
5'-most EST uC-zmflmo17407b11a1

Seq. No. 258811
Contig ID 259_1.R1011
5'-most EST fC-zmfl700355774:_FL

Seq. No. 258812
Contig ID 260_1.R1011
5'-most EST LIB3075-019-Q1-K1-C10
Method BLASTX
NCBI GI g2501850
BLAST score 1893
E value 0.0e+00
Match length 433
% identity 82

NCBI Description	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No.	258813
Contig ID	261_1.R1011
5'-most EST	uC-zmf1b73051e09a2
Method	BLASTX
NCBI GI	g2146739
BLAST score	1595
E value	1.0e-178
Match length	457
% identity	68
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No.	258814
Contig ID	262_1.R1011
5'-most EST	LIB3136-011-Q1-K1-A10
Method	BLASTX
NCBI GI	g1170871
BLAST score	1573
E value	1.0e-176
Match length	399
% identity	75
NCBI Description	MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice >gi_415315_dbj_BAA03949_ (D16499) NADP-dependent malic enzyme [Oryza sativa]

Seq. No.	258815
Contig ID	264_1.R1011
5'-most EST	pmx700083149.h1
Method	BLASTX
NCBI GI	g3402722
BLAST score	1200
E value	0.0e+00
Match length	502
% identity	77
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	258816
Contig ID	264_2.R1011
5'-most EST	uC-zmroteosinte004f11b1
Method	BLASTX
NCBI GI	g3402722
BLAST score	823
E value	2.0e-88
Match length	181
% identity	84
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	258817
Contig ID	264_4.R1011
5'-most EST	LIB3067-055-Q1-K1-G12
Method	BLASTX
NCBI GI	g3402722
BLAST score	433

E value	1.0e-42
Match length	101
% identity	76
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	258818
Contig ID	265_1.R1011
5'-most EST	zuv700353218.h1
Method	BLASTX
NCBI GI	g2911042
BLAST score	1553
E value	1.0e-173
Match length	394
% identity	77
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	258819
Contig ID	265_2.R1011
5'-most EST	uC-zmf1b73152c03b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	201
E value	1.0e-32
Match length	103
% identity	71
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	258820
Contig ID	266_1.R1011
5'-most EST	fC-zmf1700378034_FL
Method	BLASTX
NCBI GI	g2645170
BLAST score	1618
E value	0.0e+00
Match length	382
% identity	81
NCBI Description	(D50576) YY2 protein [Oryza sativa]

Seq. No.	258821
Contig ID	267_1.R1011
5'-most EST	xdb700341886.h1

Seq. No.	258822
Contig ID	269_1.R1011
5'-most EST	afb700381131.h1
Method	BLASTX
NCBI GI	g3342242
BLAST score	1840
E value	0.0e+00
Match length	463
% identity	72
NCBI Description	(AF030421) cell wall invertase; beta-fructofuranosidase; fructosidase [Triticum aestivum]

Seq. No. 258823

Contig ID	270_1.R1011
5'-most EST	clt700045156.f1
Method	BLASTX
NCBI GI	g3057120
BLAST score	1686
E value	0.0e+00
Match length	393
% identity	78
NCBI Description	(AF023159) starch synthase DULL1 [Zea mays]

Seq. No.	258824
Contig ID	271_1.R1011
5'-most EST	uC-zmflb73131e07b2
Method	BLASTX
NCBI GI	g2224915
BLAST score	909
E value	6.0e-98
Match length	243
% identity	67
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	258825
Contig ID	271_2.R1011
5'-most EST	uC-zmflb73188b07b1
Method	BLASTX
NCBI GI	g2224915
BLAST score	924
E value	1.0e-99
Match length	243
% identity	67
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	258826
Contig ID	271_3.R1011
5'-most EST	uC-zmflb73280a12b2
Method	BLASTX
NCBI GI	g2224915
BLAST score	902
E value	3.0e-97
Match length	231
% identity	71
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	258827
Contig ID	271_4.R1011
5'-most EST	uC-zmflmo17335d10b1
Method	BLASTX
NCBI GI	g2224915
BLAST score	491
E value	2.0e-49
Match length	147
% identity	63
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	258828
Contig ID	271_6.R1011
5'-most EST	uC-zmflmo17398h09a1

Seq. No.	258829
Contig ID	272_1.R1011
5'-most EST	fC-zmf1700381459_FL
Method	BLASTX
NCBI GI	g3287857
BLAST score	703
E value	6.0e-74
Match length	252
% identity	56
NCBI Description	3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA DEHYDROGENASE) (BHBD) >gi_1209052 (U32229) HbdA [Bradyrhizobium japonicum]

Seq. No.	258830
Contig ID	272_2.R1011
5'-most EST	pmx700081915.h1
Method	BLASTX
NCBI GI	g2501578
BLAST score	1298
E value	1.0e-143
Match length	313
% identity	83
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	258831
Contig ID	272_3.R1011
5'-most EST	LIB3059-058-Q1-K1-E10
Method	BLASTX
NCBI GI	g3287857
BLAST score	267
E value	3.0e-23
Match length	142
% identity	44
NCBI Description	3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA DEHYDROGENASE) (BHBD) >gi_1209052 (U32229) HbdA [Bradyrhizobium japonicum]

Seq. No.	258832
Contig ID	273_1.R1011
5'-most EST	uC-zmf1b73213e03a1
Method	BLASTX
NCBI GI	g2129550
BLAST score	1948
E value	0.0e+00
Match length	466
% identity	77
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	258833
Contig ID	273_2.R1011
5'-most EST	nbm700477567.h1

Seq. No.	258834
Contig ID	274_1.R1011
5'-most EST	uC-zmflmo17136b11b1
Method	BLASTX
NCBI GI	g135060
BLAST score	4041
E value	0.0e+00
Match length	802
% identity	97
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382) sucrose synthase [Zea mays]

Seq. No.	258835
Contig ID	274_2.R1011
5'-most EST	ymt700221147.h1
Method	BLASTX
NCBI GI	g1351136
BLAST score	4302
E value	0.0e+00
Match length	816
% identity	100
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_514946 (L22296) UDP-glucose:D-fructose 2-glucosyl-transferase [Zea mays] >gi_533252 (L33244) sucrose synthase 2 [Zea mays]

Seq. No.	258836
Contig ID	274_3.R1011
5'-most EST	LIB143-002-Q1-E1-H2
Method	BLASTX
NCBI GI	g584706
BLAST score	1952
E value	0.0e+00
Match length	404
% identity	93
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi_2130066_pir__JC5124 aspartate transaminase (EC 2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_ (D14673) aspartate aminotransferase [Oryza sativa]

Seq. No.	258837
Contig ID	274_4.R1011
5'-most EST	cjh700194011.h1
Method	BLASTX
NCBI GI	g584706
BLAST score	308
E value	1.0e-40
Match length	140

% identity	71
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi_2130066_pir__JC5124 aspartate transaminase (EC 2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_ (D14673) aspartate aminotransferase [Oryza sativa]
Seq. No.	258838
Contig ID	274_6.R1011
5'-most EST	uC-zmflmo17289d04b1
Method	BLASTX
NCBI GI	g135060
BLAST score	294
E value	2.0e-26
Match length	56
% identity	98
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382) sucrose synthase [Zea mays]
Seq. No.	258839
Contig ID	274_7.R1011
5'-most EST	xsy700208695.h1
Method	BLASTN
NCBI GI	g533251
BLAST score	254
E value	1.0e-140
Match length	340
% identity	94
NCBI Description	Zea mays (clone pSM8) sucrose synthase 2 (Sus1) gene, complete cds
Seq. No.	258840
Contig ID	274_8.R1011
5'-most EST	uC-zmflmo17198g09b1
Method	BLASTX
NCBI GI	g135060
BLAST score	360
E value	4.0e-34
Match length	82
% identity	90
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382) sucrose synthase [Zea mays]
Seq. No.	258841
Contig ID	274_30.R1011
5'-most EST	uwc700155657.h1
Method	BLASTX
NCBI GI	g741983
BLAST score	264
E value	2.0e-23
Match length	50
% identity	100

NCBI Description	sucrose synthase:ISOTYPE=2 [Zea mays]
Seq. No.	258842
Contig ID	275_1.R1011
5'-most EST	fC-zmf1700381963:_FL
Method	BLASTX
NCBI GI	g4097094
BLAST score	561
E value	3.0e-57
Match length	263
% identity	49
NCBI Description	(U45447) vacuolar proton-ATPase subunit D [Oryctolagus cuniculus]
Seq. No.	258843
Contig ID	275_2.R1011
5'-most EST	qmh700026412.f1
Seq. No.	258844
Contig ID	275_3.R1011
5'-most EST	LIB3078-056-Q1-K1-C12
Seq. No.	258845
Contig ID	275_4.R1011
5'-most EST	LIB148-017-Q1-E1-C8
Method	BLASTX
NCBI GI	g731097
BLAST score	274
E value	4.0e-24
Match length	114
% identity	52
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN) >gi_1083086_pir__A55910 subunit D vacuolar H(+)-ATPase - bovine >gi_517446 (U11927) vacuolar H-ATPase subunit D [Bos gaurus]
Seq. No.	258846
Contig ID	276_1.R1011
5'-most EST	LIB3279-059-P1-K1-G7
Method	BLASTX
NCBI GI	g4512664
BLAST score	1252
E value	1.0e-138
Match length	311
% identity	78
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
Seq. No.	258847
Contig ID	276_2.R1011
5'-most EST	fC-zmle700578607f1
Method	BLASTX
NCBI GI	g4512664
BLAST score	293
E value	2.0e-26

Match length	84
% identity	70
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	258848
Contig ID	276_3.R1011
5'-most EST	LIB3137-015-Q1-K1-B2
Method	BLASTX
NCBI GI	g4512664
BLAST score	495
E value	4.0e-50
Match length	116
% identity	81
NCBI Description	(AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi_4544471_gb_AAD22378.1_AC006580_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	258849
Contig ID	277_1.R1011
5'-most EST	LIB148-012-Q1-E1-H2

Seq. No.	258850
Contig ID	278_1.R1011
5'-most EST	LIB3075-045-Q1-K1-H12
Method	BLASTX
NCBI GI	g3885492
BLAST score	1128
E value	1.0e-126
Match length	228
% identity	97
NCBI Description	(AF063865) tapetum specific protein [Zea mays]

Seq. No.	258851
Contig ID	279_1.R1011
5'-most EST	cyk700052056.f1
Method	BLASTX
NCBI GI	g3367596
BLAST score	1289
E value	1.0e-142
Match length	370
% identity	70
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	258852
Contig ID	280_1.R1011
5'-most EST	LIB3066-014-Q1-K1-G10
Method	BLASTX
NCBI GI	g626029
BLAST score	475
E value	2.0e-47
Match length	132
% identity	65
NCBI Description	pollen allergen Lol p XI - perennial ryegrass

	>gi_1582249_prf__2118270A allergen Lol p XI [Lolium perenne]
Seq. No.	258853
Contig ID	280_2.R1011
5'-most EST	ymy700282545.h2
Method	BLASTX
NCBI GI	g626029
BLAST score	504
E value	7.0e-51
Match length	131
% identity	70
NCBI Description	pollen allergen Lol p XI - perennial ryegrass >gi_1582249_prf__2118270A allergen Lol p XI [Lolium perenne]
Seq. No.	258854
Contig ID	281_1.R1011
5'-most EST	LIB3062-025-Q1-K1-D4
Method	BLASTX
NCBI GI	g3355626
BLAST score	892
E value	1.0e-168
Match length	362
% identity	79
NCBI Description	(Y09204) histidinol-phosphate aminotransferase [Nicotiana tabacum]
Seq. No.	258855
Contig ID	282_1.R1011
5'-most EST	xjt700095261.h1
Method	BLASTX
NCBI GI	g4426627
BLAST score	1146
E value	1.0e-126
Match length	267
% identity	75
NCBI Description	(AF099969) sterol-C5(6)-desaturase homolog [Nicotiana tabacum]
Seq. No.	258856
Contig ID	282_3.R1011
5'-most EST	yne700378507.h1
Method	BLASTX
NCBI GI	g4426627
BLAST score	310
E value	3.0e-28
Match length	62
% identity	82
NCBI Description	(AF099969) sterol-C5(6)-desaturase homolog [Nicotiana tabacum]
Seq. No.	258857
Contig ID	282_5.R1011
5'-most EST	LIB3137-014-Q1-K1-A8
Seq. No.	258858

Contig ID	283_1.R1011
5'-most EST	fC-zmf1700550995_FL
Method	BLASTX
NCBI GI	g1705463
BLAST score	182
E value	2.0e-13
Match length	41
% identity	88
NCBI Description	BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201 biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi_2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi_1589016_prf__2209438A biotin synthase [Arabidopsis thaliana]

Seq. No.	258859
Contig ID	284_1.R1011
5'-most EST	uC-zmroteosinte118a10b1
Method	BLASTX
NCBI GI	g1806142
BLAST score	935
E value	1.0e-101
Match length	219
% identity	76
NCBI Description	(X97315) cdc2MsD [Medicago sativa]

Seq. No.	258860
Contig ID	285_1.R1011
5'-most EST	fC-zmf1700553370_FL
Method	BLASTX
NCBI GI	g2352084
BLAST score	370
E value	2.0e-35
Match length	110
% identity	70
NCBI Description	(U96613) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	258861
Contig ID	285_2.R1011
5'-most EST	LIB189-008-Q1-E1-E5
Method	BLASTX
NCBI GI	g2352084
BLAST score	651
E value	2.0e-68
Match length	137
% identity	89
NCBI Description	(U96613) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	258862
Contig ID	286_1.R1011
5'-most EST	LIB3075-047-Q1-K1-A5
Method	BLASTX
NCBI GI	g584777
BLAST score	298
E value	9.0e-27

Match length	76
% identity	74
NCBI Description	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1)

Seq. No.	258863
Contig ID	287_16.R1011
5'-most EST	LIB3066-010-Q1-K1-C10

Seq. No.	258864
Contig ID	287_17.R1011
5'-most EST	uC-zmflMo17086c02b1

Seq. No.	258865
Contig ID	287_19.R1011
5'-most EST	xjt700095025.h1

Seq. No.	258866
Contig ID	287_20.R1011
5'-most EST	uC-zmflb73178f04b1

Seq. No.	258867
Contig ID	287_21.R1011
5'-most EST	LIB3066-038-Q1-K1-E12

Seq. No.	258868
Contig ID	287_22.R1011
5'-most EST	uC-zmflb73413b09a1

Seq. No.	258869
Contig ID	287_23.R1011
5'-most EST	hvj700619653.h1

Seq. No.	258870
Contig ID	287_24.R1011
5'-most EST	LIB3061-044-Q1-K1-H5

Seq. No.	258871
Contig ID	287_25.R1011
5'-most EST	wty700169279.h1

Seq. No.	258872
Contig ID	287_26.R1011
5'-most EST	uC-zmflb73214g09a1
Method	BLASTN
NCBI GI	g4416300
BLAST score	92
E value	2.0e-44
Match length	261
% identity	45
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	258873
Contig ID	287_27.R1011

5'-most EST	wty700163043.h1
Seq. No.	258874
Contig ID	287_28.R1011
5'-most EST	dyk700105488.h1
Seq. No.	258875
Contig ID	287_29.R1011
5'-most EST	uC-zmrob73044h06a1
Method	BLASTN
NCBI GI	g4416300
BLAST score	200
E value	1.0e-108
Match length	330
% identity	48
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence
Seq. No.	258876
Contig ID	287_30.R1011
5'-most EST	LIB3075-025-Q1-K1-F9
Seq. No.	258877
Contig ID	287_31.R1011
5'-most EST	LIB3066-011-Q1-K1-D10
Seq. No.	258878
Contig ID	287_32.R1011
5'-most EST	LIB3078-024-Q1-K1-D5
Seq. No.	258879
Contig ID	287_33.R1011
5'-most EST	uC-zmflMo17016a02b1
Seq. No.	258880
Contig ID	287_34.R1011
5'-most EST	bdu700382968.h1
Seq. No.	258881
Contig ID	287_35.R1011
5'-most EST	uC-zmflmo17132g06b1
Seq. No.	258882
Contig ID	287_36.R1011
5'-most EST	LIB3061-005-Q1-K1-D9
Method	BLASTN
NCBI GI	g4185305
BLAST score	267
E value	1.0e-148
Match length	641
% identity	81
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes
Seq. No.	258883

Contig ID	287_37.R1011
5'-most EST	uC-zmf1b73171e05b1
Method	BLASTN
NCBI GI	g4416300
BLAST score	77
E value	4.0e-35
Match length	129
% identity	46
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	258884
Contig ID	287_38.R1011
5'-most EST	LIB3150-091-P1-N1-G1

Seq. No.	258885
Contig ID	287_39.R1011
5'-most EST	LIB3068-010-Q1-K1-H12

Seq. No.	258886
Contig ID	287_40.R1011
5'-most EST	LIB3156-013-Q1-K1-C6

Seq. No.	258887
Contig ID	287_41.R1011
5'-most EST	LIB3066-049-Q1-K1-G1
Method	BLASTN
NCBI GI	g4416300
BLAST score	160
E value	1.0e-84
Match length	429
% identity	46
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	258888
Contig ID	287_42.R1011
5'-most EST	LIB3060-004-Q1-K1-B10
Method	BLASTN
NCBI GI	g3452299
BLAST score	67
E value	3.0e-29
Match length	192
% identity	86
NCBI Description	Zea mays retrotransposon Ji-6 3' LTR, partial sequence

Seq. No.	258889
Contig ID	287_43.R1011
5'-most EST	zuv700354930.h1

Seq. No.	258890
Contig ID	287_44.R1011
5'-most EST	LIB189-027-Q1-E1-F9

Seq. No.	258891
Contig ID	287_45.R1011
5'-most EST	LIB36-003-Q1-E1-H3

Seq. No.	258892
Contig ID	287_46.R1011
5'-most EST	LIB3066-048-Q1-K1-B1

Seq. No.	258893
Contig ID	287_47.R1011
5'-most EST	wyr700240233.h1

Seq. No.	258894
Contig ID	287_48.R1011
5'-most EST	LIB3060-016-Q1-K1-B3
Method	BLASTN
NCBI GI	g4416300
BLAST score	70
E value	6.0e-31
Match length	118
% identity	45
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	258895
Contig ID	287_49.R1011
5'-most EST	LIB3116-010-Q1-K1-A1

Seq. No.	258896
Contig ID	287_50.R1011
5'-most EST	LIB148-033-Q1-E1-B9
Method	BLASTN
NCBI GI	g433038
BLAST score	61
E value	9.0e-26
Match length	81
% identity	94
NCBI Description	Zea mays W-22 clone cDNA7 retroelement PREM-1-containing mRNA

Seq. No.	258897
Contig ID	287_51.R1011
5'-most EST	LIB3066-014-Q1-K1-B11
Method	BLASTN
NCBI GI	g2832242
BLAST score	428
E value	0.0e+00
Match length	460
% identity	13
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	258898
Contig ID	287_52.R1011
5'-most EST	wyr700238654.h1
Method	BLASTN
NCBI GI	g1244652
BLAST score	152
E value	6.0e-80
Match length	244
% identity	46

NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete cds

Seq. No. 258899
Contig ID 287_53.R1011
5'-most EST LIB3060-034-Q1-K1-C8

Seq. No. 258900
Contig ID 287_54.R1011
5'-most EST LIB148-028-Q1-E1-F2
Method BLASTN
NCBI GI g433044
BLAST score 144
E value 5.0e-75
Match length 176
% identity 95
NCBI Description Zea mays W-22 clone PREM-1D retroelement PREM-1, partial sequence

Seq. No. 258901
Contig ID 287_55.R1011
5'-most EST uer700579605.h1

Seq. No. 258902
Contig ID 287_56.R1011
5'-most EST uC-zmflmo17263f12b1

Seq. No. 258903
Contig ID 287_57.R1011
5'-most EST uC-zmflmo17220g10b1

Seq. No. 258904
Contig ID 287_58.R1011
5'-most EST LIB148-022-Q1-E1-E2

Seq. No. 258905
Contig ID 287_59.R1011
5'-most EST LIB3075-028-Q1-K1-F8
Method BLASTX
NCBI GI g2429087
BLAST score 322
E value 5.0e-30
Match length 113
% identity 58
NCBI Description (L37358) lipoxygenase 2 [Hordeum vulgare]

Seq. No. 258906
Contig ID 287_60.R1011
5'-most EST uer700577816.h1
Method BLASTX
NCBI GI g2506825
BLAST score 287
E value 5.0e-26
Match length 92
% identity 63
NCBI Description LIPOXYGENASE 1 >gi_532572 (L35931) lipoxygenase 1 [Hordeum vulgare] >gi_1094924_prf__2107185A lipoxygenase [Hordeum

vulgare]

Seq. No.	258907
Contig ID	287_61.R1011
5'-most EST	uC-zmflmo17341a04b1
Method	BLASTN
NCBI GI	g4416300
BLAST score	54
E value	2.0e-21
Match length	104
% identity	45
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	258908
Contig ID	287_62.R1011
5'-most EST	xsy700207329.h1

Seq. No.	258909
Contig ID	287_63.R1011
5'-most EST	LIB3066-013-Q1-K1-C7

Seq. No.	258910
Contig ID	287_64.R1011
5'-most EST	uC-zmflb73195e06b1
Method	BLASTN
NCBI GI	g22447
BLAST score	37
E value	2.0e-11
Match length	37
% identity	100
NCBI Description	Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No.	258911
Contig ID	287_65.R1011
5'-most EST	LIB3059-035-Q1-K1-E10

Seq. No.	258912
Contig ID	287_66.R1011
5'-most EST	uC-zmflB73025f11b2

Seq. No.	258913
Contig ID	287_67.R1011
5'-most EST	LIB3136-002-P1-K1-H7
Method	BLASTX
NCBI GI	g126401
BLAST score	373
E value	3.0e-36
Match length	87
% identity	79
NCBI Description	LIPOXYGENASE L-2 >gi_100690_pir__S23454 lipoxygenase (EC 1.13.11.12) L-2 - rice >gi_20267_emb_CAA45738_ (X64396) lipoxygenase [Oryza sativa]

Seq. No.	258914
Contig ID	287_68.R1011
5'-most EST	uC-zmflmo17125b02b1

Seq. No.	258915
Contig ID	287_69.R1011
5'-most EST	LIB36-021-Q1-E1-C1
Seq. No.	258916
Contig ID	287_70.R1011
5'-most EST	uC-zmflmo17069f07b1
Seq. No.	258917
Contig ID	287_71.R1011
5'-most EST	fwa700098016.h1
Seq. No.	258918
Contig ID	287_72.R1011
5'-most EST	wyr700241024.h1
Method	BLASTN
NCBI GI	g4416300
BLAST score	118
E value	1.0e-59
Match length	250
% identity	44
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence
Seq. No.	258919
Contig ID	287_73.R1011
5'-most EST	mwy700439844.h1
Seq. No.	258920
Contig ID	287_74.R1011
5'-most EST	uC-zmflmo17289h10b1
Method	BLASTN
NCBI GI	g433041
BLAST score	127
E value	7.0e-65
Match length	323
% identity	92
NCBI Description	Zea mays W-22 clone PREM-1B retroelement PREM-1, partial sequence
Seq. No.	258921
Contig ID	287_75.R1011
5'-most EST	LIB3150-072-P2-K1-D1
Method	BLASTN
NCBI GI	g433038
BLAST score	131
E value	2.0e-67
Match length	203
% identity	91
NCBI Description	Zea mays W-22 clone cDNA7 retroelement PREM-1-containing mRNA
Seq. No.	258922
Contig ID	287_76.R1011
5'-most EST	uC-zmflmo17022g07b1

Seq. No.	258923
Contig ID	287_77.R1011
5'-most EST	ntr700075965.h1
Method	BLASTX
NCBI GI	g3204159
BLAST score	285
E value	3.0e-66
Match length	184
% identity	63
NCBI Description	(AJ006523) coatomer, beta-prime subunit [Drosophila melanogaster] >gi_3204161_emb_CAA07085_ (AJ006524) coatomer, beta-prime subunit [Drosophila melanogaster]

Seq. No.	258924
Contig ID	287_78.R1011
5'-most EST	uC-zmflb73278a03b1

Seq. No.	258925
Contig ID	287_79.R1011
5'-most EST	mwy700440461.h1
Method	BLASTX
NCBI GI	g2506825
BLAST score	187
E value	8.0e-14
Match length	40
% identity	85
NCBI Description	LIPOXYGENASE 1 >gi_532572 (L35931) lipoxygenase 1 [Hordeum vulgare] >gi_1094924_prf__2107185A lipoxygenase [Hordeum vulgare]

Seq. No.	258926
Contig ID	287_80.R1011
5'-most EST	LIB3067-039-Q1-K1-G7
Method	BLASTX
NCBI GI	g3645899
BLAST score	325
E value	4.0e-30
Match length	76
% identity	80
NCBI Description	(U68408) 5' end not determined experimentally [Zea mays]

Seq. No.	258927
Contig ID	287_81.R1011
5'-most EST	fC-zmle700421516:_FL

Seq. No.	258928
Contig ID	287_82.R1011
5'-most EST	LIB84-006-Q1-E1-A8

Seq. No.	258929
Contig ID	287_83.R1011
5'-most EST	nbm700470175.h1

Seq. No.	258930
Contig ID	287_84.R1011
5'-most EST	nbm700477431.h1

Seq. No.	258931
Contig ID	287_85.R1011
5'-most EST	uC-zmflmo17159a03b1
Method	BLASTN
NCBI GI	g4416300
BLAST score	109
E value	3.0e-54
Match length	270
% identity	47
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	258932
Contig ID	287_86.R1011
5'-most EST	uC-zmflmo17054b08b1

Seq. No.	258933
Contig ID	287_87.R1011
5'-most EST	uC-zmflmo17044c05b1
Method	BLASTN
NCBI GI	g22447
BLAST score	85
E value	1.0e-39
Match length	307
% identity	89
NCBI Description	Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No.	258934
Contig ID	287_88.R1011
5'-most EST	LIB3060-032-Q1-K1-B3
Method	BLASTN
NCBI GI	g433038
BLAST score	139
E value	6.0e-72
Match length	199
% identity	92
NCBI Description	Zea mays W-22 clone cDNA7 retroelement PREM-1-containing mRNA

Seq. No.	258935
Contig ID	287_89.R1011
5'-most EST	LIB148-030-Q1-E1-B9

Seq. No.	258936
Contig ID	287_90.R1011
5'-most EST	mwy700441301.h1
Method	BLASTN
NCBI GI	g4140643
BLAST score	63
E value	1.0e-26
Match length	106
% identity	91
NCBI Description	Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	258937
Contig ID	287_91.R1011

5'-most EST	LIB3060-042-Q1-K1-G9
Seq. No.	258938
Contig ID	287_92.R1011
5'-most EST	LIB3136-018-Q1-K1-H12
Method	BLASTN
NCBI GI	g4416300
BLAST score	117
E value	7.0e-59
Match length	195
% identity	45
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence
Seq. No.	258939
Contig ID	287_93.R1011
5'-most EST	pwr700450135.h1
Method	BLASTN
NCBI GI	g22447
BLAST score	213
E value	1.0e-116
Match length	344
% identity	91
NCBI Description	Zea mays ZMPMS2 gene for 19 kDa zein protein
Seq. No.	258940
Contig ID	287_94.R1011
5'-most EST	uC-zmflmo17257b02b1
Method	BLASTN
NCBI GI	g433043
BLAST score	89
E value	3.0e-42
Match length	177
% identity	88
NCBI Description	Zea mays W-22 clone PREM-1E retroelement PREM-1, partial sequence
Seq. No.	258941
Contig ID	287_95.R1011
5'-most EST	LIB143-040-Q1-E1-A10
Method	BLASTN
NCBI GI	g4416300
BLAST score	95
E value	8.0e-46
Match length	131
% identity	47
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence
Seq. No.	258942
Contig ID	287_96.R1011
5'-most EST	mwy700440838.h1
Seq. No.	258943
Contig ID	287_97.R1011
5'-most EST	uC-zmflm017211f10b1
Method	BLASTN

NCBI GI	g433043
BLAST score	94
E value	3.0e-45
Match length	125
% identity	95
NCBI Description	Zea mays W-22 clone PREM-1E retroelement PREM-1, partial sequence
Seq. No.	258944
Contig ID	287_98.R1011
5'-most EST	uer700577023.h1
Seq. No.	258945
Contig ID	287_99.R1011
5'-most EST	uC-zmflB73042b12b1
Seq. No.	258946
Contig ID	287_100.R1011
5'-most EST	ntr700076363.h1
Seq. No.	258947
Contig ID	287_101.R1011
5'-most EST	wty700170905.h1
Seq. No.	258948
Contig ID	287_102.R1011
5'-most EST	uC-zmflm017209f06b1
Method	BLASTN
NCBI GI	g717080
BLAST score	150
E value	1.0e-78
Match length	293
% identity	88
NCBI Description	Zea mays glyceraldehyde-3-phosphate dehydrogenase (GapC4) gene, promoter region
Seq. No.	258949
Contig ID	287_103.R1011
5'-most EST	cyk700050287.f1
Method	BLASTN
NCBI GI	g433038
BLAST score	171
E value	3.0e-91
Match length	227
% identity	94
NCBI Description	Zea mays W-22 clone cDNA7 retroelement PREM-1-containing mRNA
Seq. No.	258950
Contig ID	287_104.R1011
5'-most EST	wty700163395.h1
Seq. No.	258951
Contig ID	287_105.R1011
5'-most EST	LIB148-047-Q1-E1-B11
Seq. No.	258952

Contig ID	287_106.R1011
5'-most EST	LIB3068-041-Q1-K1-F8
Seq. No.	258953
Contig ID	287_107.R1011
5'-most EST	LIB3066-016-Q1-K1-B3
Seq. No.	258954
Contig ID	287_108.R1011
5'-most EST	dyk700104303.h1
Seq. No.	258955
Contig ID	288_1.R1011
5'-most EST	fC-zmle700421615_FL
Method	BLASTX
NCBI GI	g2191136
BLAST score	157
E value	6.0e-11
Match length	75
% identity	48
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]
Seq. No.	258956
Contig ID	289_1.R1011
5'-most EST	LIB3157-013-Q1-K1-B12
Method	BLASTX
NCBI GI	g1838961
BLAST score	301
E value	5.0e-27
Match length	117
% identity	62
NCBI Description	(Y10994) acyl carrier protein [Casuarina glauca]
Seq. No.	258957
Contig ID	290_1.R1011
5'-most EST	fC-zmle700421740_FL
Method	BLASTX
NCBI GI	g4127688
BLAST score	264
E value	4.0e-30
Match length	100
% identity	64
NCBI Description	(AJ006065) isochorismate synthase [Catharanthus roseus]
Seq. No.	258958
Contig ID	291_1.R1011
5'-most EST	fC-zmle700421804_FL
Seq. No.	258959
Contig ID	292_1.R1011
5'-most EST	fC-zmle700421971:_FL
Method	BLASTX
NCBI GI	g3236253
BLAST score	539

E value	5.0e-55
Match length	215
% identity	51
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	258960
Contig ID	293_1.R1011
5'-most EST	fC-zmle700422028:_FL

Seq. No.	258961
Contig ID	295_1.R1011
5'-most EST	uC-zmflmo17277d11a1
Method	BLASTX
NCBI GI	g1706082
BLAST score	908
E value	1.0e-133
Match length	312
% identity	75
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	258962
Contig ID	295_2.R1011
5'-most EST	vux700160383.h1
Method	BLASTN
NCBI GI	g474391
BLAST score	47
E value	2.0e-17
Match length	115
% identity	85
NCBI Description	H.vulgare L. (Alexis) Serine carboxypeptidase II-3 mRNA

Seq. No.	258963
Contig ID	296_1.R1011
5'-most EST	uC-zmroteosinte102f12b2
Method	BLASTX
NCBI GI	g1477480
BLAST score	363
E value	3.0e-34
Match length	109
% identity	66
NCBI Description	(U40341) carbamoyl phosphate synthetase large chain [Arabidopsis thaliana]

Seq. No.	258964
Contig ID	297_1.R1011
5'-most EST	fC-zmle700423970_FL
Method	BLASTX
NCBI GI	g2586083
BLAST score	225
E value	3.0e-18

Match length	118
% identity	40
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	258965
Contig ID	298_1.R1011
5'-most EST	uC-zmflb73080g04b2
Method	BLASTX
NCBI GI	g4587513
BLAST score	1126
E value	1.0e-123
Match length	329
% identity	64
NCBI Description	(AC007060) Contains eukaryotic protein kinase domain PF_00069. [Arabidopsis thaliana]

Seq. No.	258966
Contig ID	298_2.R1011
5'-most EST	uC-zmflb73061a05b1
Method	BLASTX
NCBI GI	g4539330
BLAST score	175
E value	3.0e-12
Match length	144
% identity	34
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	258967
Contig ID	298_4.R1011
5'-most EST	fdz701160622.h1

Seq. No.	258968
Contig ID	299_1.R1011
5'-most EST	uC-zmflmo17020g10b1
Method	BLASTX
NCBI GI	g3695005
BLAST score	1883
E value	0.0e+00
Match length	364
% identity	100
NCBI Description	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]

Seq. No.	258969
Contig ID	299_2.R1011
5'-most EST	uC-zmflb73191c10b1
Method	BLASTX
NCBI GI	g2117355
BLAST score	1557
E value	1.0e-174
Match length	499
% identity	62
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain precursor - potato >gi_587562_emb_CAA56520_ (X80236) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	258970
Contig ID	299_4.R1011
5'-most EST	LIB3136-003-Q1-K1-C8
Method	BLASTX
NCBI GI	g3929545
BLAST score	289
E value	8.0e-26
Match length	76
% identity	79
NCBI Description	(AF067194) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No.	258971
Contig ID	299_5.R1011
5'-most EST	xmt700263855.h1
Method	BLASTX
NCBI GI	g4220446
BLAST score	337
E value	2.0e-31
Match length	91
% identity	73
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]

Seq. No.	258972
Contig ID	300_1.R1011
5'-most EST	tzu700201602.h1
Method	BLASTX
NCBI GI	g3242708
BLAST score	729
E value	6.0e-77
Match length	291
% identity	50
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	258973
Contig ID	301_1.R1011
5'-most EST	fC-zmle700426373:_FL
Method	BLASTX
NCBI GI	g1418990
BLAST score	180
E value	6.0e-13
Match length	68
% identity	54
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	258974
Contig ID	302_1.R1011
5'-most EST	uC-zmflmo17053c04b1
Method	BLASTX
NCBI GI	g1085973
BLAST score	1055

E value	1.0e-115
Match length	228
% identity	85
NCBI Description	isopentyl pyrophosphate isomerase - Clarkia breweri (fragment) >gi_572635_emb_CAA57947_ (X82627) isopentenyl pyrophosphate isomerase [Clarkia breweri]

Seq. No.	258975
Contig ID	302_2.R1011
5'-most EST	LIB3066-042-Q1-K1-E8
Method	BLASTX
NCBI GI	g1213442
BLAST score	306
E value	2.0e-27
Match length	93
% identity	69
NCBI Description	(U48961) isopentenyl pyrophosphate isomerase [Arabidopsis thaliana]

Seq. No.	258976
Contig ID	302_3.R1011
5'-most EST	uC-zmflmo17047c05a1
Method	BLASTX
NCBI GI	g1085973
BLAST score	564
E value	8.0e-58
Match length	125
% identity	83
NCBI Description	isopentyl pyrophosphate isomerase - Clarkia breweri (fragment) >gi_572635_emb_CAA57947_ (X82627) isopentenyl pyrophosphate isomerase [Clarkia breweri]

Seq. No.	258977
Contig ID	303_1.R1011
5'-most EST	uC-zmroteosinte045h11b2
Method	BLASTX
NCBI GI	g4006829
BLAST score	596
E value	2.0e-61
Match length	182
% identity	65
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	258978
Contig ID	303_2.R1011
5'-most EST	LIB3136-003-Q1-K1-E10
Method	BLASTX
NCBI GI	g1168470
BLAST score	307
E value	9.0e-52
Match length	144
% identity	77
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	258979
Contig ID	304_1.R1011
5'-most EST	fC-zmle700426721:_FL

Seq. No.	258980
Contig ID	306_1.R1011
5'-most EST	fC-zmst700623122a1
Method	BLASTX
NCBI GI	g4538976
BLAST score	384
E value	9.0e-37
Match length	156
% identity	49
NCBI Description	(AL049487) sucrose-phosphate synthase-like protein [Arabidopsis thaliana]

Seq. No.	258981
Contig ID	307_1.R1011
5'-most EST	fC-zmle700427304:_FL
Method	BLASTX
NCBI GI	g2997591
BLAST score	554
E value	1.0e-56
Match length	147
% identity	71
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	258982
Contig ID	308_1.R1011
5'-most EST	tzu700201874.h1
Method	BLASTX
NCBI GI	g2462834
BLAST score	333
E value	1.0e-30
Match length	142
% identity	47
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	258983
Contig ID	308_2.R1011
5'-most EST	vux700158343.h1
Method	BLASTX
NCBI GI	g2462834
BLAST score	333
E value	8.0e-31
Match length	145
% identity	46
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	258984
Contig ID	309_1.R1011
5'-most EST	uC-zmflmo17134b09a1
Method	BLASTX
NCBI GI	g3256035
BLAST score	271

E value	9.0e-24
Match length	90
% identity	56
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No.	258985
Contig ID	310_1.R1011
5'-most EST	LIB143-012-Q1-E1-B6
Method	BLASTX
NCBI GI	g2688828
BLAST score	648
E value	2.0e-67
Match length	334
% identity	42
NCBI Description	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No.	258986
Contig ID	311_1.R1011
5'-most EST	LIB3180-015-P2-M1-B3
Method	BLASTX
NCBI GI	g1616661
BLAST score	2380
E value	0.0e+00
Match length	484
% identity	95
NCBI Description	(U49388) adenylosuccinate synthetase [Zea mays]

Seq. No.	258987
Contig ID	312_1.R1011
5'-most EST	fC-zmle700578414_FL
Method	BLASTX
NCBI GI	g1903357
BLAST score	326
E value	4.0e-30
Match length	134
% identity	47
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	258988
Contig ID	313_1.R1011
5'-most EST	uC-zmflb73407f11a2
Method	BLASTX
NCBI GI	g2245077
BLAST score	238
E value	6.0e-20
Match length	57
% identity	74
NCBI Description	(Z97343) glucanase homolog [Arabidopsis thaliana]

Seq. No.	258989
Contig ID	314_1.R1011
5'-most EST	uC-zmflb73205g09b2
Method	BLASTX
NCBI GI	g2632252

BLAST score 1581
E value 1.0e-177
Match length 330
% identity 92
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 258990
Contig ID 314_2.R1011
5'-most EST uC-zmf1B73008e08b1
Method BLASTX
NCBI GI g2632254
BLAST score 373
E value 1.0e-35
Match length 89
% identity 87
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 258991
Contig ID 314_4.R1011
5'-most EST xtd700282379.h2
Method BLASTX
NCBI GI g2632254
BLAST score 352
E value 3.0e-33
Match length 82
% identity 84
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 258992
Contig ID 315_1.R1011
5'-most EST LIB84-008-Q1-E1-H4
Method BLASTX
NCBI GI g1362021
BLAST score 182
E value 6.0e-13
Match length 69
% identity 58
NCBI Description zink finger protein 7 - Arabidopsis thaliana >gi_790685 (L39650) zinc finger protein [Arabidopsis thaliana] >gi_2213609 (AC000103) F21J9.3 [Arabidopsis thaliana]

Seq. No. 258993
Contig ID 315_2.R1011
5'-most EST LIB3078-039-Q1-K1-D7
Method BLASTX
NCBI GI g1362017
BLAST score 149
E value 2.0e-09
Match length 58
% identity 53
NCBI Description zinc finger protein 4 - Arabidopsis thaliana >gi_790679 (L39647) zinc finger protein [Arabidopsis thaliana]

Seq. No. 258994
Contig ID 316_1.R1011
5'-most EST wyr700244154.h1
Method BLASTX

NCBI GI	g4314378
BLAST score	678
E value	6.0e-71
Match length	280
% identity	46
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	258995
Contig ID	316_2.R1011
5'-most EST	LIB3062-022-Q1-K1-G12

Seq. No.	258996
Contig ID	316_3.R1011
5'-most EST	uC-zmflmo17221b01a1

Seq. No.	258997
Contig ID	316_4.R1011
5'-most EST	LIB3150-012-Q1-N1-H11

Seq. No.	258998
Contig ID	317_1.R1011
5'-most EST	fC-zmro700451410_FL
Method	BLASTN
NCBI GI	g4416300
BLAST score	88
E value	1.0e-41
Match length	336
% identity	84
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	258999
Contig ID	317_2.R1011
5'-most EST	uC-zmf1b73056g01b1
Method	BLASTN
NCBI GI	g4416300
BLAST score	95
E value	1.0e-45
Match length	383
% identity	84
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	259000
Contig ID	318_1.R1011
5'-most EST	fC-zmro700570160_FL
Method	BLASTX
NCBI GI	g2493493
BLAST score	301
E value	5.0e-27
Match length	117
% identity	48
NCBI Description	SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1) >gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324 aa]

Seq. No.	259001
Contig ID	318_2.R1011
5'-most EST	fC-zmro700451901:_FL
Method	BLASTX
NCBI GI	g3738328
BLAST score	414
E value	3.0e-40
Match length	149
% identity	50
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	259002
Contig ID	319_1.R1011
5'-most EST	fC-zmro700452834:_FL
Method	BLASTX
NCBI GI	g2507246
BLAST score	355
E value	6.0e-34
Match length	66
% identity	100
NCBI Description	COMPLEMENT FACTOR D PRECURSOR (C3 CONVERTASE ACTIVATOR) (PROPERDIN FACTOR D) (ADIPSIN) (ENDOGENOUS VASCULAR ELASTASE) >gi_2118079_pir__I55608 endogenous vascular elastase - rat >gi_693722_bbs_157144 (S73894) endogenous vascular elastase, EVE=serine proteinase adipsin homolog [rats, Sprague-Dawley, pulmonary arteries, Peptide, 263 aa] [Rattus sp.]

Seq. No.	259003
Contig ID	320_1.R1011
5'-most EST	rvl700456136.h1
Method	BLASTX
NCBI GI	g1619300
BLAST score	305
E value	2.0e-27
Match length	153
% identity	40
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	259004
Contig ID	321_1.R1011
5'-most EST	fC-zmro700569668_FL
Method	BLASTX
NCBI GI	g4038030
BLAST score	696
E value	3.0e-73
Match length	172
% identity	72
NCBI Description	(AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No.	259005
Contig ID	323_1.R1011
5'-most EST	xsy700211828.h1
Method	BLASTX
NCBI GI	g2914710

BLAST score	908
E value	1.0e-110
Match length	358
% identity	56
NCBI Description	(AC003974) putative beta-D-galactosidase [Arabidopsis thaliana]

Seq. No.	259006
Contig ID	324_1.R1011
5'-most EST	uC-zmflmo17403e01a1
Method	BLASTX
NCBI GI	g2809262
BLAST score	464
E value	3.0e-47
Match length	216
% identity	49
NCBI Description	(AC002560) F21B7.31 [Arabidopsis thaliana]

Seq. No.	259007
Contig ID	325_1.R1011
5'-most EST	uwc700151077.h1
Method	BLASTX
NCBI GI	g3913182
BLAST score	935
E value	1.0e-101
Match length	251
% identity	74
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_2239258_emb_CAA74070_ (Y13733) cinnamyl alcohol dehydrogenase [Zea mays]

Seq. No.	259008
Contig ID	325_2.R1011
5'-most EST	fC-zmro700570469_FL
Method	BLASTN
NCBI GI	g3097280
BLAST score	295
E value	1.0e-165
Match length	353
% identity	99
NCBI Description	Zea mays mRNA for cinnamyl alcohol dehydrogenase

Seq. No.	259009
Contig ID	325_3.R1011
5'-most EST	uC-zmf1b73369d05a1
Method	BLASTX
NCBI GI	g3097281
BLAST score	448
E value	3.0e-44
Match length	120
% identity	78
NCBI Description	(AJ005702) cinnamyl alcohol dehydrogenase [Zea mays]

Seq. No.	259010
Contig ID	326_1.R1011
5'-most EST	fC-zmro700570704r1
Method	BLASTX

NCBI GI	g1175395
BLAST score	185
E value	2.0e-13
Match length	131
% identity	31
NCBI Description	HYPOTHETICAL 14.1 KD PROTEIN C31A2.02 IN CHROMOSOME I >gi_2130413_pir__S58099 hypothetical protein SPAC31A2.02 - fission yeast (Schizosaccharomyces pombe) >gi_914880_emb_CAA90460_ (Z50113) unknown [Schizosaccharomyces pombe]

Seq. No.	259011
Contig ID	327_1.R1011
5'-most EST	LIB3059-054-Q1-K1-E11
Method	BLASTX
NCBI GI	g3775995
BLAST score	716
E value	2.0e-75
Match length	190
% identity	66
NCBI Description	(AJ010461) RNA helicase [Arabidopsis thaliana]

Seq. No.	259012
Contig ID	327_2.R1011
5'-most EST	nbm700478039.h1

Seq. No.	259013
Contig ID	328_1.R1011
5'-most EST	fC-zmro700571573_FL
Method	BLASTX
NCBI GI	g4538947
BLAST score	983
E value	1.0e-106
Match length	288
% identity	42
NCBI Description	(AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	259014
Contig ID	329_1.R1011
5'-most EST	LIB3059-030-Q1-K1-B11
Method	BLASTX
NCBI GI	g1706695
BLAST score	210
E value	5.0e-16
Match length	284
% identity	28
NCBI Description	PHOSPHOMEVALONATE KINASE >gi_1362436_pir__S57588 phosphomevalonate kinase (EC 2.7.4.2) - yeast (Saccharomyces cerevisiae) >gi_887601_emb_CAA90191_ (Z49939) Erg8p [Saccharomyces cerevisiae]

Seq. No.	259015
Contig ID	329_2.R1011
5'-most EST	LIB3137-029-Q1-K1-H9
Method	BLASTX
NCBI GI	g1706695

BLAST score	162
E value	5.0e-11
Match length	103
% identity	39
NCBI Description	PHOSPHOMEVALONATE KINASE >gi_1362436_pir__S57588 phosphomevalonate kinase (EC 2.7.4.2) - yeast (Saccharomyces cerevisiae) >gi_887601_emb_CAA90191_ (Z49939) Erg8p [Saccharomyces cerevisiae]

Seq. No.	259016
Contig ID	329_3.R1011
5'-most EST	fC-zmf1700341257b1

Seq. No.	259017
Contig ID	330_1.R1011
5'-most EST	fC-zmro700571850_FL
Method	BLASTX
NCBI GI	g3688209
BLAST score	361
E value	5.0e-34
Match length	114
% identity	61
NCBI Description	(AJ010093) MAP3K beta 1 protein kinase [Brassica napus]

Seq. No.	259018
Contig ID	331_1.R1011
5'-most EST	fC-zmro700572286_FL
Method	BLASTX
NCBI GI	g2655031
BLAST score	324
E value	8.0e-30
Match length	64
% identity	91
NCBI Description	(AF019297) starch synthase isoform zSTSII-2 [Zea mays]

Seq. No.	259019
Contig ID	331_2.R1011
5'-most EST	uC-zmf1b73212b10a1
Method	BLASTX
NCBI GI	g2655031
BLAST score	626
E value	4.0e-65
Match length	121
% identity	95
NCBI Description	(AF019297) starch synthase isoform zSTSII-2 [Zea mays]

Seq. No.	259020
Contig ID	332_1.R1011
5'-most EST	fC-zmro700572502_FL
Method	BLASTX
NCBI GI	g629602
BLAST score	155
E value	6.0e-10
Match length	55
% identity	49
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition

protein [Brassica oleracea]

Seq. No.	259021
Contig ID	333_1.R1011
5'-most EST	fC-zmro700572669_FL
Method	BLASTX
NCBI GI	g4539330
BLAST score	568
E value	1.0e-69
Match length	193
% identity	70
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	259022
Contig ID	334_1.R1011
5'-most EST	xmt700258227.h1
Method	BLASTX
NCBI GI	g4417286
BLAST score	644
E value	6.0e-67
Match length	206
% identity	62
NCBI Description	(AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No.	259023
Contig ID	334_2.R1011
5'-most EST	uC-zmflb73062d01b1
Method	BLASTX
NCBI GI	g114200
BLAST score	169
E value	1.0e-11
Match length	48
% identity	67
NCBI Description	SHIKIMATE KINASE PRECURSOR >gi_100253_pir__S21584 shikimate kinase precursor - tomato >gi_19349_emb_CAA45121_ (X63560) shikimate kinase precursor [Lycopersicon esculentum]

Seq. No.	259024
Contig ID	334_3.R1011
5'-most EST	LIB3116-014-Q1-K1-D1
Method	BLASTN
NCBI GI	g3821794
BLAST score	39
E value	2.0e-12
Match length	51
% identity	94
NCBI Description	Zea mays gene encoding protein kinase CK2 alpha subunit

Seq. No.	259025
Contig ID	334_5.R1011
5'-most EST	LIB189-029-Q1-E1-A12

Seq. No.	259026
Contig ID	334_6.R1011
5'-most EST	uC-zmflmo17331c04a1
Method	BLASTX

NCBI GI	g4417286
BLAST score	153
E value	5.0e-10
Match length	63
% identity	51
NCBI Description	(AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No.	259027
Contig ID	335_1.R1011
5'-most EST	LIB3150-107-P2-K1-E5

Seq. No.	259028
Contig ID	335_2.R1011
5'-most EST	uC-zmflb73080b12a1

Seq. No.	259029
Contig ID	335_4.R1011
5'-most EST	uC-zmflmo17257c08b1

Seq. No.	259030
Contig ID	335_5.R1011
5'-most EST	uC-zmflMo17084h05b1

Seq. No.	259031
Contig ID	335_6.R1011
5'-most EST	uC-zmroteosinte022d04b1

Seq. No.	259032
Contig ID	335_9.R1011
5'-most EST	LIB3067-055-Q1-K1-G7

Seq. No.	259033
Contig ID	335_10.R1011
5'-most EST	LIB3157-019-Q1-K1-D7

Seq. No.	259034
Contig ID	336_1.R1011
5'-most EST	uC-zmflb73242f04b1
Method	BLASTX
NCBI GI	g1815681
BLAST score	1048
E value	1.0e-114
Match length	223
% identity	85
NCBI Description	(U85246) expansin [Oryza sativa]

Seq. No.	259035
Contig ID	336_2.R1011
5'-most EST	LIB36-007-Q1-E1-G3
Method	BLASTX
NCBI GI	g1815681
BLAST score	691
E value	1.0e-72
Match length	263
% identity	86
NCBI Description	(U85246) expansin [Oryza sativa]

Seq. No. 259036
Contig ID 336_3.R1011
5'-most EST LIB3069-017-Q1-K1-B3
Method BLASTX
NCBI GI g1041702
BLAST score 437
E value 5.0e-43
Match length 122
% identity 67
NCBI Description (U30476) expansin At-EXP1 [Arabidopsis thaliana]

Seq. No. 259037
Contig ID 336_4.R1011
5'-most EST LIB3062-059-Q1-K1-G3

Seq. No. 259038
Contig ID 336_5.R1011
5'-most EST uC-zmflb73130b02a1

Seq. No. 259039
Contig ID 336_6.R1011
5'-most EST LIB3062-057-Q1-K1-D11
Method BLASTX
NCBI GI g1041710
BLAST score 950
E value 1.0e-103
Match length 281
% identity 65
NCBI Description (U30477) expansin Os-EXP2 [Oryza sativa]

Seq. No. 259040
Contig ID 336_7.R1011
5'-most EST uC-zmflmo17291h04a1

Seq. No. 259041
Contig ID 336_8.R1011
5'-most EST fC-zmfl700550656a1
Method BLASTX
NCBI GI g3747132
BLAST score 350
E value 8.0e-33
Match length 99
% identity 65
NCBI Description (AF096776) expansin [Lycopersicon esculentum]

Seq. No. 259042
Contig ID 337_1.R1011
5'-most EST fC-zmro700573083_FL
Method BLASTX
NCBI GI g2494417
BLAST score 397
E value 4.0e-38
Match length 198
% identity 86
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
>gi_1364071_pir__S57717 fructose-1, 6-bisphosphatase (EC

3.1.3.11) - sugarcane hybrid H65-7052
>gi_895909_emb_CAA61409.1_ (X89006) fructose-1,
6-bisphosphatase [Saccharum hybrid cultivar H65-7052]

Seq. No.	259043
Contig ID	337_2.R1011
5'-most EST	uC-zmroB73020b07b1
Method	BLASTX
NCBI GI	g3913640
BLAST score	819
E value	1.0e-126
Match length	248
% identity	91
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041775_dbj_BAA25422_ (AB007193) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	259044
Contig ID	338_1.R1011
5'-most EST	uC-zmflmo17312b01b1
Method	BLASTX
NCBI GI	g1362162
BLAST score	2167
E value	0.0e+00
Match length	478
% identity	82
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	259045
Contig ID	338_2.R1011
5'-most EST	xsy700213883.h1
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	8.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	259046
Contig ID	338_3.R1011
5'-most EST	cat700017682.r1
Method	BLASTX
NCBI GI	g122085
BLAST score	589
E value	8.0e-61
Match length	136
% identity	88

NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]
Seq. No.	259047
Contig ID	338_4.R1011
5'-most EST	LIB3069-004-Q1-K1-H5
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	8.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]
Seq. No.	259048
Contig ID	338_5.R1011
5'-most EST	xsy700209683.h1
Method	BLASTX
NCBI GI	g122087
BLAST score	536
E value	2.0e-54
Match length	127
% identity	86
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_

(X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	259049
Contig ID	338_6.R1011
5'-most EST	LIB3150-043-Q1-N1-H5
Method	BLASTX
NCBI GI	g417103
BLAST score	623
E value	4.0e-65
Match length	124
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	259050
Contig ID	338_7.R1011
5'-most EST	LIB3076-036-Q1-K1-E4
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	7.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	259051
Contig ID	338_8.R1011
5'-most EST	ntr700074133.h1
Method	BLASTX
NCBI GI	g417103
BLAST score	679

E value	6.0e-71
Match length	270
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	259052
Contig ID	338_9.R1011
5'-most EST	uC-zmroteosinte086d05b1
Method	BLASTX
NCBI GI	g122087
BLAST score	673
E value	1.0e-70
Match length	136
% identity	100
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	259053
Contig ID	338_10.R1011
5'-most EST	uC-zmflb73069e07b1
Method	BLASTX
NCBI GI	g417103
BLAST score	665
E value	1.0e-69
Match length	133
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone

H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	259054
Contig ID	338_11.R1011
5'-most EST	LIB3279-011-P1-K1-G5
Method	BLASTX
NCBI GI	g122085
BLAST score	446
E value	2.0e-44
Match length	90
% identity	100
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	259055
Contig ID	338_16.R1011
5'-most EST	LIB3067-010-Q1-K1-C10
Method	BLASTX
NCBI GI	g122085
BLAST score	585
E value	2.0e-60
Match length	136
% identity	87
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis

thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	259056
Contig ID	338_17.R1011
5'-most EST	uC-zmroteosinte036b03b1
Method	BLASTX
NCBI GI	g122085
BLAST score	670
E value	2.0e-70
Match length	136
% identity	99
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	259057
Contig ID	338_18.R1011
5'-most EST	pmx700086563.h1
Method	BLASTX
NCBI GI	g122085
BLAST score	661
E value	3.0e-69
Match length	136
% identity	99
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	259058
Contig ID	338_19.R1011
5'-most EST	LIB3069-039-Q1-K1-A11
Method	BLASTX
NCBI GI	g122087
BLAST score	585
E value	2.0e-60
Match length	135
% identity	87
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	259059
Contig ID	338_20.R1011
5'-most EST	LIB3150-035-Q1-N1-E2
Method	BLASTX

NCBI GI	g122085
BLAST score	670
E value	2.0e-70
Match length	136
% identity	99
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]
Seq. No.	259060
Contig ID	338_21.R1011
5'-most EST	LIB3069-044-Q1-K1-G9
Method	BLASTX
NCBI GI	g417103
BLAST score	478
E value	1.0e-54
Match length	142
% identity	84
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	259061
Contig ID	338_22.R1011
5'-most EST	LIB3070-015-Q1-N1-B12
Method	BLASTX
NCBI GI	g122085
BLAST score	580
E value	8.0e-60
Match length	134
% identity	87
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	259062
Contig ID	338_28.R1011
5'-most EST	uC-zmroteosinte100a03b2
Method	BLASTX
NCBI GI	g1362162
BLAST score	437
E value	2.0e-62
Match length	125
% identity	93
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	259063
Contig ID	339_1.R1011
5'-most EST	wty700169889.h1
Method	BLASTX
NCBI GI	g3024122
BLAST score	1910
E value	0.0e+00
Match length	434
% identity	92

NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No.	259064
Contig ID	339_2.R1011
5'-most EST	uwc700150248.h1
Method	BLASTX
NCBI GI	g3024122
BLAST score	1889
E value	0.0e+00
Match length	392
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No.	259065
Contig ID	339_3.R1011
5'-most EST	uC-zmflb73126e10b1
Method	BLASTX
NCBI GI	g4204265
BLAST score	919
E value	7.0e-99
Match length	449
% identity	48
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	259066
Contig ID	339_4.R1011
5'-most EST	uC-zmflb73347d11a1
Method	BLASTX
NCBI GI	g1076389
BLAST score	2717
E value	0.0e+00
Match length	587
% identity	89
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	259067
Contig ID	339_5.R1011
5'-most EST	LIB189-026-Q1-E1-H12
Method	BLASTX
NCBI GI	g1709000
BLAST score	418
E value	2.0e-40
Match length	86
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare]

Seq. No.	259068
Contig ID	339_6.R1011

5'-most EST	LIB3150-112-P2-K1-A1
Method	BLASTX
NCBI GI	g1076389
BLAST score	1008
E value	1.0e-109
Match length	230
% identity	24
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	259069
Contig ID	339_7.R1011
5'-most EST	uC-zmflb73086e11b2
Method	BLASTX
NCBI GI	g3024122
BLAST score	713
E value	2.0e-75
Match length	140
% identity	96
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No.	259070
Contig ID	339_8.R1011
5'-most EST	LIB84-014-Q1-E1-D11
Method	BLASTX
NCBI GI	g461595
BLAST score	393
E value	9.0e-38
Match length	145
% identity	56
NCBI Description	ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II) >gi_479533_pir__S34473 H+-transporting ATP synthase (EC 3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_ (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]

Seq. No.	259071
Contig ID	339_9.R1011
5'-most EST	ymt700219056.h1
Method	BLASTX
NCBI GI	g4240035
BLAST score	497
E value	6.0e-50
Match length	134
% identity	74
NCBI Description	(AB018588) ZmGR1b [Zea mays]

Seq. No.	259072
Contig ID	339_11.R1011
5'-most EST	LIB143-034-Q1-E1-B7

Seq. No.	259073
Contig ID	339_15.R1011
5'-most EST	uC-zmflb73250g06a2

Seq. No.	259074
Contig ID	339_18.R1011
5'-most EST	LIB36-017-Q1-E1-E6
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	259075
Contig ID	339_19.R1011
5'-most EST	LIB3059-014-Q1-K1-D7

Seq. No.	259076
Contig ID	339_22.R1011
5'-most EST	xsy700211827.h1
Method	BLASTX
NCBI GI	g1709000
BLAST score	411
E value	4.0e-40
Match length	116
% identity	73
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare]

Seq. No.	259077
Contig ID	339_27.R1011
5'-most EST	cat700019427.r1
Method	BLASTX
NCBI GI	g1076390
BLAST score	172
E value	4.0e-12
Match length	44
% identity	70
NCBI Description	protein phosphatase 2A pDF2 - Arabidopsis thaliana >gi_683504_emb_CAA57529_ (X82003) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	259078
Contig ID	339_34.R1011
5'-most EST	xsy700207473.h1
Method	BLASTN
NCBI GI	g4240032
BLAST score	70
E value	2.0e-31
Match length	110
% identity	92
NCBI Description	Zea mays ZmGR1a mRNA, complete cds

Seq. No.	259079
Contig ID	340_1.R1011
5'-most EST	wty700169676.h1
Method	BLASTX

NCBI GI	g116054
BLAST score	1254
E value	1.0e-138
Match length	290
% identity	82
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) >gi_280393_pir__A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean >gi_169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]

Seq. No.	259080
Contig ID	341_1.R1011
5'-most EST	fC-zmro700574335_FL
Method	BLASTX
NCBI GI	g2827715
BLAST score	345
E value	5.0e-36
Match length	208
% identity	45
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	259081
Contig ID	342_1.R1011
5'-most EST	fC-zmro700574433_FL

Seq. No.	259082
Contig ID	343_1.R1011
5'-most EST	tfd700570920.h1
Method	BLASTX
NCBI GI	g2565305
BLAST score	1856
E value	0.0e+00
Match length	393
% identity	89
NCBI Description	(AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No.	259083
Contig ID	343_2.R1011
5'-most EST	xjt700095358.h1
Method	BLASTX
NCBI GI	g710308
BLAST score	523
E value	2.0e-53
Match length	135
% identity	72
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	259084
Contig ID	344_1.R1011
5'-most EST	fC-zmro700575270_FL
Method	BLASTX
NCBI GI	g1402918
BLAST score	381
E value	2.0e-36
Match length	101

% identity	70
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	259085
Contig ID	345_1.R1011
5'-most EST	fC-zmro700575714_FL
Method	BLASTX
NCBI GI	g2522210
BLAST score	558
E value	4.0e-57
Match length	201
% identity	49
NCBI Description	(AF023132) choline monooxygenase [Beta vulgaris]

Seq. No.	259086
Contig ID	346_1.R1011
5'-most EST	fC-zmro700753209_FL
Method	BLASTX
NCBI GI	g130186
BLAST score	1389
E value	1.0e-154
Match length	313
% identity	88
NCBI Description	PHYTOCHROME A >gi_82715_pir__JQ0382 phytochrome A - maize

Seq. No.	259087
Contig ID	346_3.R1011
5'-most EST	xdb700341355.h1
Method	BLASTX
NCBI GI	g130186
BLAST score	222
E value	6.0e-18
Match length	46
% identity	100
NCBI Description	PHYTOCHROME A >gi_82715_pir__JQ0382 phytochrome A - maize

Seq. No.	259088
Contig ID	347_1.R1011
5'-most EST	fC-zmro700832108d4
Method	BLASTX
NCBI GI	g4154352
BLAST score	392
E value	1.0e-37
Match length	241
% identity	39
NCBI Description	(AF110333) PrMC3 [Pinus radiata]

Seq. No.	259089
Contig ID	348_1.R1011
5'-most EST	fC-zmro700830011_FL
Method	BLASTX
NCBI GI	g2833378
BLAST score	544
E value	2.0e-55
Match length	171

% identity	62
NCBI Description	HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis thaliana] >gi_1582383_prf__2118367A hexokinase [Arabidopsis thaliana]

Seq. No.	259090
Contig ID	349_1.R1011
5'-most EST	fC-zmro700830067_FL
Method	BLASTX
NCBI GI	g4538929
BLAST score	476
E value	4.0e-47
Match length	287
% identity	49
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	259091
Contig ID	350_1.R1011
5'-most EST	fC-zmro700830312a1
Method	BLASTX
NCBI GI	g3702332
BLAST score	342
E value	1.0e-31
Match length	193
% identity	34
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	259092
Contig ID	351_1.R1011
5'-most EST	fC-zmro700830348_FL
Method	BLASTX
NCBI GI	g3901012
BLAST score	1101
E value	1.0e-120
Match length	254
% identity	77
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	259093
Contig ID	352_1.R1011
5'-most EST	fC-zmro700830504_FL
Method	BLASTX
NCBI GI	g4240116
BLAST score	417
E value	9.0e-41
Match length	88
% identity	85
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	259094
Contig ID	353_1.R1011
5'-most EST	fC-zmro700830907_FL
Method	BLASTX

NCBI GI g4191788
BLAST score 690
E value 1.0e-72
Match length 165
% identity 78
NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No. 259095
Contig ID 354_1.R1011
5'-most EST fC-zmro700831325_FL
Method BLASTX
NCBI GI g2088653
BLAST score 691
E value 9.0e-73
Match length 223
% identity 58
NCBI Description (AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]

Seq. No. 259096
Contig ID 355_1.R1011
5'-most EST fC-zmro700831537_FL
Method BLASTX
NCBI GI g3851001
BLAST score 896
E value 1.0e-113
Match length 233
% identity 87
NCBI Description (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]

Seq. No. 259097
Contig ID 356_1.R1011
5'-most EST fC-zmro700831955_FL
Method BLASTX
NCBI GI g3850630
BLAST score 700
E value 1.0e-73
Match length 199
% identity 62
NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]

Seq. No. 259098
Contig ID 356_2.R1011
5'-most EST fC-zmro700831544_FL
Method BLASTX
NCBI GI g3850630
BLAST score 419
E value 7.0e-41
Match length 120
% identity 57
NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]

Seq. No. 259099
Contig ID 357_1.R1011
5'-most EST fC-zmro700831637_FL

Method	BLASTX
NCBI GI	g1168470
BLAST score	926
E value	1.0e-100
Match length	259
% identity	73
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	259100
Contig ID	359_1.R1011
5'-most EST	fC-zmro700832181_FL
Method	BLASTX
NCBI GI	g4585966
BLAST score	1225
E value	1.0e-135
Match length	296
% identity	79
NCBI Description	(AC005287) Putative dihyrdolipoamide acetyltransferase [Arabidopsis thaliana]

Seq. No.	259101
Contig ID	360_1.R1011
5'-most EST	fC-zmro700832243_FL
Method	BLASTX
NCBI GI	g3335378
BLAST score	378
E value	5.0e-36
Match length	158
% identity	51
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	259102
Contig ID	361_1.R1011
5'-most EST	fC-zmro700832459_FL
Method	BLASTX
NCBI GI	g2129770
BLAST score	434
E value	1.0e-42
Match length	126
% identity	64
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No.	259103
Contig ID	362_1.R1011
5'-most EST	fC-zmro700832582_FL
Method	BLASTX
NCBI GI	g2959732
BLAST score	353

E value	3.0e-33
Match length	71
% identity	89
NCBI Description	(Y13649) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	259104
Contig ID	363_1.R1011
5'-most EST	fC-zmro700832613_FL
Method	BLASTX
NCBI GI	g3169883
BLAST score	305
E value	1.0e-27
Match length	136
% identity	47
NCBI Description	(AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No.	259105
Contig ID	364_1.R1011
5'-most EST	fC-zmro700832966_FL
Method	BLASTX
NCBI GI	g3204134
BLAST score	707
E value	2.0e-74
Match length	182
% identity	68
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	259106
Contig ID	365_1.R1011
5'-most EST	fC-zmro700833257_FL
Method	BLASTX
NCBI GI	g2494329
BLAST score	376
E value	1.0e-35
Match length	294
% identity	34
NCBI Description	GLUCAN 1,3-BETA-GLUCOSIDASE PRECURSOR (EXO-1,3-BETA-GLUCANASE) >gi_1150694_emb_CAA86952_ (Z46872) exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase [Yarrowia lipolytica]

Seq. No.	259107
Contig ID	366_1.R1011
5'-most EST	fC-zmro700833374_FL
Method	BLASTX
NCBI GI	g1872521
BLAST score	303
E value	3.0e-27
Match length	113
% identity	36
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	259108
Contig ID	367_1.R1011
5'-most EST	fC-zmro700833817_FL
Method	BLASTX
NCBI GI	g2789434
BLAST score	252
E value	3.0e-21
Match length	163
% identity	41
NCBI Description	(AB001389) CLB1 [Lycopersicon esculentum]

Seq. No.	259109
Contig ID	368_1.R1011
5'-most EST	fC-zmro700833909_FL
Method	BLASTX
NCBI GI	g3128195
BLAST score	204
E value	8.0e-16
Match length	43
% identity	88
NCBI Description	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]

Seq. No.	259110
Contig ID	369_1.R1011
5'-most EST	fC-zmro700833923_FL
Method	BLASTX
NCBI GI	g3540200
BLAST score	237
E value	2.0e-19
Match length	186
% identity	35
NCBI Description	(AC004260) Similar to TINY [Arabidopsis thaliana]

Seq. No.	259111
Contig ID	370_1.R1011
5'-most EST	fC-zmro700834004_FL
Method	BLASTX
NCBI GI	g2979553
BLAST score	511
E value	1.0e-51
Match length	166
% identity	59
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	259112
Contig ID	371_1.R1011
5'-most EST	fC-zmro700834049_FL
Method	BLASTX
NCBI GI	g1915974
BLAST score	1416
E value	1.0e-157
Match length	319
% identity	86

NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi_2102693 (U64818) fructokinase [Lycopersicon esculentum]
Seq. No.	259113
Contig ID	371_2.R1011
5'-most EST	fC-zmro700832903d4
Method	BLASTX
NCBI GI	g1052973
BLAST score	406
E value	1.0e-39
Match length	97
% identity	81
NCBI Description	(U37838) fructokinase [Beta vulgaris]
Seq. No.	259114
Contig ID	372_1.R1011
5'-most EST	fC-zmro700834170_FL
Method	BLASTX
NCBI GI	g2088653
BLAST score	684
E value	7.0e-72
Match length	241
% identity	53
NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]
Seq. No.	259115
Contig ID	372_2.R1011
5'-most EST	fC-zmro700833740d4
Method	BLASTX
NCBI GI	g2088653
BLAST score	253
E value	1.0e-21
Match length	87
% identity	57
NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]
Seq. No.	259116
Contig ID	373_1.R1011
5'-most EST	fC-zmro700835672:_FL
Method	BLASTX
NCBI GI	g3450842
BLAST score	894
E value	3.0e-96
Match length	269
% identity	62
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]
Seq. No.	259117
Contig ID	374_1.R1011
5'-most EST	fC-zmro700835718:_FL
Method	BLASTX
NCBI GI	g2829275
BLAST score	649
E value	7.0e-68